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(54) Title: 83 HUMAN SECRETED PROTEINS

#### (57) Abstract

The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.

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|---|--|---|---|---|---|--|--|

### 83 Human Secreted Proteins

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#### Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and their production.

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#### Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include the commercially valuable human insulin, interferon. Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoeitin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that

encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using secreted proteins or the genes that encode them.

#### Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, 5 antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners 10 of the polypeptides.

#### Detailed Description

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The following definitions are provided to facilitate understanding of certain **Definitions** terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide"

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refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH<sub>2</sub>PO<sub>4</sub>; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking

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reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

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Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural

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processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS -STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

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#### Polynucleotides and Polypeptides of the Invention FEATURES OF PROTEIN ENCODED BY GENE NO: 1

This gene is expressed in a broad variety of tissues and cell types.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, liver cancer. Similarly, polypeptides and antibodies directed to

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these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., hepatic, cancerous and wounded tissues) or bodily fluids (e.g., bile, lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:99 as residues: Ser-34 to Arg-39, Leu-50 to Ser-55.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:11 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1747 of SEQ ID NO:11, b is an integer of 15 to 1761, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where the b is greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 2 25

Preferred polypeptides encoded by this gene comprise the following amino

MEQTWTRDYFAEDDGEMVPRTSHTAAFLSDTKDRGPPVQSQIWRSGEKVPFVQTYSLRAFEKPPQVQTQALRDFEKHLNDLKKENFSLKLXIYFLEERMQQ KYEASREDIYKRNTELKVEVESLKRELQDKKQHLDKTWADVENLNSQNEA ELRRQFEERHXETEHVYELLENKXQLLQEESRLAKNEAARMAALVEAEKEC NLELSEKLKGVTKNWEDVPGDQVKPDQYTEALAQRDK (SEQ ID NO:188) or MVPRTSHTAAFLSDTKDRGPPVQSQIWRSGEKVPFVQTYSLRAFEKPPQVQTQALRDFEKHLNDLKKENFSLKLXIYFLEERMQQKYEASREDIYKRNTELK VEVESLKRELQDKKQHLDKTWADVENLNSQNEAELRRQFEERHXETEHVY ELLENKXQLLQEESRLAKNEAARMAALVEAEKECNLELSEKLKGVTKNWE

DVPGDQVKPDQYTEALAQRDK (SEQ ID NO:187). Polynucleotides encoding these polypeptides are also provided.

This gene is expressed primarily in infant brain and to a lesser extent in a large variety of other tissues, organs and cell types.

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Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, various forms of congentital mental retartation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., developmental, cancerous and wounded tissues) or bodily fluids (e.g., amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:100 as residues: Met-1 to Arg-22, Leu-46 to Arg-52, Asn-64 to Gln-70. 20

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:12 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1505 of SEQ ID NO:12, b is an integer of 15 to 1519, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where the b is greater than or equal to a + 14.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 3

Preferred polypeptide encoded by this gene comprise the following amino acid sequence:

IRHELLPALHLQAHDAAYNLLFFASGGGKFNYQGTKRWLEDNLDHTGERP

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RVGVGVPRWWCRGEAXRPRGCHGGSQEAQREGRGPLPGPHPPRQLSVSC RLQPASGQCGLRAVPGHRGPGQQPAPAXVRPXREGTLQHAFXRELETVAA HQFPEVRFSMVHKRINLAEDVLAWEHERFAIRRLPAFTLSHLESHRDGQRS SIMDVRSRVDSKTLIRLPQPPKVLGLRV (SEQ ID NO:189). Polynucleotides encoding such polypeptides are also provided. This gene is believed to reside on chromosome 19. Thus, polynucleotides related to this gene are useful as chromosome markers in linkage analysis for chromosome 19.

This gene is expressed primarily in microvascular endothelial cells and to a lesser extent in in a variety of other cell types including activated T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, blood circulatory diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., vascular, and blood, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:13 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1057 of SEQ ID NO:13, b is an integer of 15 to 1071, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where the b is greater than or equal to a + 14.

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The gene encoding the disclosed cDNA sequence is believed to reside on chromosome 22. Accordingly, polynucleotides related to this invention are useful in linkage analysis as markers for chromosome 22.

This gene is expressed primarily in a variety of cell types of muscle and bone origin.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoporosis or any of a variety of disease that involve wasting to bone or muscle. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and muscular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., musculoskeletal, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:102 as residues: Lys-81 20 to Thr-92, Arg-168 to Tyr-176, Gly-199 to Scr-216.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:14 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 941 of SEQ ID NO:14, b is an integer of 15 to 955, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where the b is greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 5 35

This gene is expressed primarily in the brain.

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Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, various brain disorders including mood disorders, memory disorders, depression, and seizures. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., neural, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:103 as residues: Ser-62 to Cys-67.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:15 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1494 of SEQ ID NO:15, b is an integer of 15 to 1508, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where the b is greater than or equal to a + 14.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 6

When tested against PC12 cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) pathway. Thus, it is likely that this gene activates sensory neuron cells through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jaks-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation. This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1.

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This gene is expressed primarily in small intestine, and to a lesser extent, in fetal liver and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissuc(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, intestinal cancers, premalignancies, and development disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.gastrointesinal, developing, or cancerous and wounded tissues) or bodily fluids (e.g.amniotic fluid, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of intestinal cancers and premalignancies, or ulcers, intestinal infections or other conditions arising from disorders of the gastrointesinal system. Alternatively, based upon the detected EGR activity in sensory neurons may suggest that the protein product of this gene is useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:16 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is 35 cumbersome. Accordingly, preferably excluded from the present invention are one

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or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1992 of SEQ ID NO:16, b is an integer of 15 to 2006, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where the b is greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 7

The translation product of this gene was shown to have homology to the human LAK-4p which is thought to be involved in T-cell activation as this gene is specifically expressed during such a response (See Genebank Accession No.gnllPIDld1025089 (AB002405)). Preferred polypeptides comprise the following amino acid sequence:

IYLNIQVVRGQRKVICLLKEQISNEGEDKIFLINKLHSIY (SEQ ID NO:190), ERKEREERSRVGTTEEAAAPPALLTDE (SEQ I D NO:191), and/or RHEMENT 15 (SEQ ID NO:192),. Also preferred are the polynucleotides encoding these polypeptides.

This gene is expressed primarily in several types of leukocytes, thymus, bone marrow, and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune system disorders, particularly of the leukocytes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:105 as residues: Gln-38 to Asp-45, Glu-58 to Arg-67.

The protein product of the gene, based upon its homology to the human immune-specific LAK-4p protein, in addition to its tissue distribution in leukocytes, is likely to be a modulator of the immune system and could be used in a variety of

theraputic situations which require modulation of immune cell production such as leukemias and in protection of hematoprogenitors during chemotherapy. Additionally, the protein product of this gene is useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in thymus and bone marrow indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an 10 agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have 15 commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and 20 accessible through sequence databases. Some of these sequences are related to SEQ ID NO:17 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more 25 polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 531 of SEQ ID NO:17, b is an integer of 15 to 545, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where the b is greater than or equal to a + 14. 30

# FEATURES OF PROTEIN ENCODED BY GENE NO: 8

This gene is expressed primarily in lymphocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as 35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but

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are not limited to, diseases of the immune system, particularly of the lymphocytes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in lymphocytes indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:18 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present 35 invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 588 of SEQ ID NO:18, b is an integer of 15 to 602, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where the b is greater than or equal to a+14.

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### FEATURES OF PROTEIN ENCODED BY GENE NO: 9

This gene is expressed primarily in the human embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, dvelopmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.developing, differentiating, or cancerous and wounded tissues) or bodily fluids (e.g.amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:19 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 573 of SEQ ID NO:19, b is an integer of 15 to 587, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:19, and where the b is greater than or equal to a+14.

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## FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in the human embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, reproductive and developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. developing, differentiating, or cancerous and wounded tissues) or bodily fluids (e.g. amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:108 as residues: Asn-6 to Ser-13.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:20 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present

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invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 630 of SEQ ID NO:20, b is an integer of 15 to 644, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where the b is greater than or equal to a+14.

# FEATURES OF PROTEIN ENCODED BY GENE NO: 11

This gene is expressed primarily in the human embryo and the prostate. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental and reproductive disorders, particularly with prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and urogenital systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.developmental, reproductive, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Alternatively, expression within the prostate indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of prostate cancer, and related reproductive disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are

related to SEQ ID NO:21 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1243 of SEQ ID NO:21, b is an integer of 15 to 1257, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where the b is greater than or equal to a + 14.

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### FEATURES OF PROTEIN ENCODED BY GENE NO: 12

This gene is expressed primarily in the human embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, Developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.developmental, or cancerous and wounded tissues) or bodily fluids (e.g. amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:110 as residues: Trp-6 to Arg-13.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the

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above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:22 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 527 of SEQ ID NO:22, b is an integer of 15 to 541, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where the b is greater than or equal to a + 14.

# FEATURES OF PROTEIN ENCODED BY GENE NO: 13

This gene is expressed primarily in the human embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, reproductive and developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. developmental, or cancerous and wounded tissues) or bodily fluids (e.g. amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the

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protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:23 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 553 of SEQ ID NO:23, b is an integer of 15 to 567, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where the b is greater than or equal to a + 14.

# FEATURES OF PROTEIN ENCODED BY GENE NO: 14

This gene maps to chromosome 11, and therefore, may be used as a marker in linkage analysis for chromosome 11.

This gene is expressed primarily in immune cells, particularly T cells and dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders, particularly immunodeficiences such as AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation

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of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including 5 arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and 10 committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these 15 sequences are related to SEQ ID NO:24 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence 20 described by the general formula of a-b, where a is any integer between 1 to 572 of SEQ ID NO:24, b is an integer of 15 to 586, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where the b is greater than or equal to a + 14. 25

# FEATURES OF PROTEIN ENCODED BY GENE NO: 15

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This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in the brain and, to a lesser extent, in prostate and kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the brain and CNS, such as Alzheimer's and Parkinson's disease. Similarly, polypeptides and antibodies directed to these

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polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, urogenital, or cancerous and wounded tissues) or bodily fluids (e.g.seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the tissue distribution in kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:25 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from 30 the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1496 of SEQ ID NO:25, b is an integer of 15 to 1510, where both a and b correspond to the positions of nucleotide 35

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residues shown in SEQ ID NO:25, and where the b is greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 16 5

This gene was found to have homology to both the human ni06c07.s1 and mouse Mpgc60 cDNAs which are specifically expressed in intestinal tissue (See Genebank Accession Nos AA526969 and gblY11505lMMMPGC60, respectively). As such, it is probable that the translation product of this gene is useful for the diagnosis, treatment, and/or prevention of various gastrointestinal disorders and afflictions.

This gene is expressed primarily in multiple tissues, including the brain, breast, and kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders involving the brain and central nervous system, such as Alzheimer's and Parkinson's, and reproductive and gastrointestinal disorders. Also disorders of the breast and kidney, including cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and central nervous system also the urogenital system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, endothelial, hepatic, and mammary, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, bile, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:114 as residues: Pro-3 30 to Pro-9.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome. schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors,

including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, considering the homology to intestinal-specific proteins may suggest that the translation product of this gene is useful for the diagnosis, treatment, and/or prevention of various gastrointestinal disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:26 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 521 of SEQ ID NO:26, b is an integer of 15 to 535, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where the b is greater than or equal to a + 14.

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 17

This gene maps to chromosome 19, and therefore, may be used as a marker in linkage analysis for chromosome 19.

This gene is expressed in multiple tissues, particularly brain and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the brain and central nervous system, such as Alzheimer's and Parkinson's, in addition to reproductive and developmental disorders. Also disorders of the reproductive system Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, central nervous system, and the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, reproductive, or cancerous and wounded tissues) or bodily fluids (e.g.amniotic

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fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:115 as residues: Pro-6 to Glu-35, Ser-47 to Glu-52, Gly-67 to Trp-73, Arg-85 to Asn-90, Asn-114 to Asn-119, Thr-134 to Ser-141, Asn-250 to Glu-260.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the tissue distribution in placenta indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders since development relies on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be 20 involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ 25 ID NO:27 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula 30 of a-b, where a is any integer between 1 to 1259 of SEQ ID NO:27, b is an integer of 15 to 1273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where the b is greater than or equal to a + 14. 35

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 18

The translation product of this gene was found to have homology to several collagen proteins.

This gene is expressed primarily in cells of the immune system, including monocytes and neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders affecting the immune systems such as AIDS and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.EGE, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in immune cells combined with its homology to collagen would suggest that this protein may also be important in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid, and would healing disorders. Alternatively, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils and monocytes indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including

arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:28 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence 15 described by the general formula of a-b, where a is any integer between 1 to 766 of SEQ ID NO:28, b is an integer of 15 to 780, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where the b is greater than or equal to a + 14.

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 19

This gene is expressed primarily in hepatocellular tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hepatoma, and other disorders of the liver. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the liver, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.hepatic, or cancerous and wounded tissues) or bodily fluids (e.g.bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those

comprising a sequence shown in SEQ ID NO:117 as residues: Glu-33 to Glu-56, Thr-75 to Cys-81.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). The tissue distribution in hepatic tumors indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the 10 protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:29 and may have been publicly available prior to conception of the present invention. Preferably, such related 15 polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 805 of SEQ ID NO:29, b is an integer of 15 to 819, where both a and b 20 correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where the b is greater than or equal to a + 14.

#### 25 FEATURES OF PROTEIN ENCODED BY GENE NO: 20

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This gene is expressed primarily in apoptotic T cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic and immune diseases, or cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.hematopoietic, immune or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having

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such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for 20 the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:30 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related 25 sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 594 of SEQ ID NO:30, b is an integer of 15 to 608, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where the b is 30 greater than or equal to a + 14.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 21

The translation product of this gene shares sequence homology with mouse erythroid ankyrin protein which is thought to be important in linking the spectrinbased membrane skeleton to the plasma membrane in red blood cells. As such, the

translation product of this gene may show utility in the treatment and/or diagnosis of various hematopoietic disorders involving structural anomalies such as thalassemia and sickle-cell anemia syndromes (See Genebank Accession No. gil311822). When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon-sensitive responsive element) pathway. Thus, it is likely that this gene activates kindey cells through the Jaks-STAT signal transduction pathway. The ISRE is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

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This gene is expressed primarily in colon cancer cells and, to a lesser extent, in pancreatic and testical tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers and tumors of the urogenital, hematopoietic, or endocrine systems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive and repruductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.hematopoietic, urogenital, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:119 as residues: Met-1 to Gly-6, Lys-13 to Tyr-18, Asp-23 to Asp-28, Leu-55 to Glu-60, Pro-148 to Gly-155.

The tissue distribution combined with the observed ISRE activity indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within tumor tissues and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Additionally, the homology to a structural protein in hematopoietic cells and tissues indicates that this protein may play a role in the proliferation, differentiation, and/or

survival of hematopoietic cell lineages. In such an event, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoietic lineages from early hematopoietic stem and committed progenitor cells. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could 5 again be useful in cancer therapy. Alternatively, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addisonís disease, Cushingís Syndrome, and disorders and/or cancers of the pancrease (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., 10 hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-,hypoparathyroidism), hypothallamus, and testes. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence 15 databases. Some of these sequences are related to SEQ ID NO:31 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a 20 nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1203 of SEQ ID NO:31, b is an integer of 15 to 1217, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where the b is greater than or equal to a + 14. 25

# FEATURES OF PROTEIN ENCODED BY GENE NO: 22

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This gene maps to chromosome 19, and therefore, may be used as a marker in linkage analysis for chromosome 19.

This gene is expressed primarily in umbilical vein endothelial cells and, to a lesser extent, in human adipose.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions:reproductive or metabolic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential

identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.reproductive, or cancerous and wounded tissues) or bodily fluids (e.g.amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

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The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus, this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Alternatively, expression in adipose tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, prevention, and/or treatment of various metabolic disorders such as Tay-Sachs disease, phenylkenonuria, galactosemia, porphyrias, Hurler's syndrome, or disorders related to lipid metabolism. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:32 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present 25 invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 751 of SEQ ID NO:32, b is an integer of 15 to 765, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and 30 where the b is greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 23 35

This gene is expressed primarily in bone marrow stromal cells, and, to a lesser extent, in epithelial-TNF alpha induced cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, integumentary and hematopoietic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid 10 and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

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The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of 15 hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, 20 inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, expression in cells induced by epithelial TNF-alpha indicates that polynucleotides and polypeptides corresponding to this gene are useful for the 25 diagnosis and treatment of cancer and other proliferative disorders. Expression within differentiating tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Additionally, the expression in hematopoietic cells and tissues indicates that this protein may play a role in the proliferation, differentiation, and/or survival of 30 hematopoietic cell lineages. In such an event, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoietic lineages from early hematopoietic stem and committed progenitor cells. Similarly, embryonic development also involves 35 decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could

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again be useful in cancer therapy. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:33 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 738 of SEQ ID NO:33, b is an integer of 15 to 752, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and 10 where the b is greater than or equal to a + 14.

# FEATURES OF PROTEIN ENCODED BY GENE NO: 24

This gene maps to chromosome 1, and therefore, may be used as a marker 15 in linkage analysis for chromosome 1.

This gene is expressed primarily in brain, and, to a lesser extent, in ovary and activated T-cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions:immune deficiencies and brain degenerative diseases, in addition to reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, and reproductive, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:122 as residues: Glu-2 to Glu-13, Pro-23 to Cys-36, Glu-47 to Ser-56, Val-64 to Pro-69, Val-106 to Asn-113, Ser-128 to Ala-134, Ser-155 to Thr-163, Lys-176 to Phe-188, Leu-192 to Asp-207, Leu-209 to Gly-232, Glu-262 to Asn-269, Thr-274 to Lys-279, Lys-284 to Gly-294, Pro-309 to Cys-314. Phe-35 318 to Lys-337.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic 5 disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, female reproductive disorders, or disorders of the cardiovascular system. 10 Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:34 and may have been publicly available prior to conception of the present 15 invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2251 of SEQ ID NO:34, b is an integer 20 of 15 to 2265, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where the b is greater than or equal to a + 14.

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#### FEATURES OF PROTEIN ENCODED BY GENE NO: 25

The translation product of this gene shares sequence homology with a mouse fat-specific protein FSP27 which is thought to be important in adipose differentiation (See Genebank Accession No. pirlA42445|A42445). One embodiment of this gene comprises polypeptides of the following amino acid sequence:

RKLSTGPFSACKPRATCCFTSCYLQQLLDATEDGHPPKGKASSLIPTCLKIL Q (SEQ ID NO:193), TSCYLQQLLDATEDGHPPKGKASSLIPTC (SEQ ID NO:194), and/or CCGAKRIMKEALHWALFSMQATGHV (SEQ ID NO:195). An additional embodiment is the polynucleotides encoding these polypeptides. This gene maps to chromosome 3, and therefore, may be used as a marker in linkage analysis for chromosome 3.

This gene is expressed primarily in adipose and to a lesser extent in small intestine and a few other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, adipose related disorders, including lipid metabolism disorders, and obesity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of adipose tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. adipose and gastrointestinal, or cancerous, or wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:123 as residues: Arg-30 to Gln-41.

The tissue distribution in adipose tissue combined with the homology to ASP27 indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of adipose related disorders, particularly hyper- and hypolidemias, Tay-Sachs, atherosclerosis, and obesity. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:35 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 629 of SEQ ID NO:35, b is an integer of 15 to 643, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where the b is greater than or equal to a + 14.

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The translation product of this gene was shown to have homology to a the human KIAA0427 protein, novel, brain-specific protein that may be important in brain development (See Genebank Accession No.gnllPIDld1025779 (AB007887)). One embodiment of this gene comprises polypeptides of the following amino acid

5 sequence:
PPAGATSPGRIIXPXSAVLIPSPVKSYRGWLVMGEPSREEYKIQSFDAETQQ
LLKTALKDPGAVDLEKVA
NVIVDHSLQDCVFSKEAGRMXYAIIQAESKQAGQSV
FRRGLLNRLQQEYQAREQLXARSLQGWVCYVTFICNIFDYLRVNNMPMM
10 ALVNPVYDCLFRLAQPDSLSKEEEVDCLVLQLHRVGEQLEK (SEQ ID
NO:196), PGRIIXPXSAVLIPSPVKSYRGWL (SEQ ID NO:197)
KQAGQSVFRRGLL NRLQQEYQAREQ (SEQ ID NO:198), and/or
YDCLFRLAQPDSLSKEEEVDC (SEQ ID NO:199),. An additional embodiment is
the polynucleotides encoding these polypeptides.

This gene is expressed primarily in hematopoiesis related tissues and cell types and to a lesser extent in brain and a few cancer cell lines and tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, neural, andinflammatory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, immune, cancerous, or wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:124 as residues: Met-1 to Met-6. Lys-50 to Arg-59.

The tissue distribution in brain combined with the homology to a novel brain-specific human protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic

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disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors. including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the tissue distribution in hematopoetic tissue indicates that polynucleotides and polypeptides 5 corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene 10 product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid 15 arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and 20 committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these 25 sequences are related to SEQ ID NO:36 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence 30 described by the general formula of a-b, where a is any integer between 1 to 1288 of SEQ ID NO:36, b is an integer of 15 to 1302, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where the b is greater than or equal to a + 14.

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#### FEATURES OF PROTEIN ENCODED BY GENE NO: 27

The translation product of this gene was shown to have homology to the rat mitochondrial brown-fat uncoupling protein which is an uncoupling protein specific to mitochondrial brown fat and is thought to play an integral role in the

thermogenesis of this tissue (See Genebank Accession No.P04633 ). One embodiment of this gene comprises polypeptides of the following amino acid sequence:

MKRTSVNPQTLCEARPAGXSQQPLSLDSEAPRGGVAPPRLQGPPPHQRVHL TLECTTHPTVGKASV

10 LGPCLLLLSCPRAPAGPPPPPHSRVRAGGCRPWARREGH
CRPLGADTDTSRICHGRRPFSL (SEQ ID NO:200),
MSLPAAPAGRLSPLYWRSS
NTRSQLSLLWELGHFFTRCCRRPHPNPHLPALSVCRCHILHKIMLWEPS
SPLLPALP (SEQ ID NO:201), and/or

MTSPGQGRAGRRGDEGSHNMILCKIWQR
HTLRAGRWGLGWGRRQHRVKKCPSSHSKESCDRVFELLQYKGES
RPAGAA GRDIIWFP (SEQ ID NO:202). An additional embodiment is the polynucleotides encoding these polypeptides.

This gene is expressed primarily in hematopoietic tissues and neuronal tissues and to a lesser extent in some cancer and other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, neural, and/or lipid metabolism disorders and/or diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neuronal tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, adipose, hematopoietic, and cancerous, or wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:125 as residues: Glu-11 to Ser-17.

The tissue distribution in neural tissue combined with the homology to a protein specific to adipose tissue indicates that polynucleotides and polypeptides

corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, preception, and particularly neural disorders involving anomylous lipid metabolism. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental

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disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, considering the tissue distribution in hematopoetic tissue, indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or

chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:37 and may have been publicly available prior to conception of the present

invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 991 of SEQ ID NO:37, b is an integer of 15 to 1005, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where the b is greater than or equal to a + 14.

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The translation product of this gene was shown to have homology to the serine protease PfSP6 N-terminal fragment (See Genebank Accession No. W01189) which may show utility in treatment and/or prevention of various insect or worm infestations, and/or diseases. One embodiment of this gene comprises polypeptides of the following amino acid sequence: PSLRGPKAGAPPRWRPL (SEQ ID NO:203), NLVDPPXCRNSARETLKLGRVEVSI (SEQ ID NO:204), KAGAPPR (SEQ ID NO:205), and/or CRNSAR (SEQ ID NO:206). An additional embodiment is the polynucleotides encoding these polypeptides.

This gene is expressed primarily in breast lymph node and to a lesser extent in some other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, and reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast lymph node, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.immune, reproductive, cancerous, or wounded tissues) or bodily fluids (e.g.lymph, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in breast lymph nodes indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or

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immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:38 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 594 of SEQ ID NO:38, b is an integer of 15 to 608, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:38, and where the b is greater than or equal to a + 14.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed primarily in breast lymph node, and to a lesser 20 extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, and reproductive diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast lymph node, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.immune, reproductive, cancerous, or wounded tissues) or bodily fluids (e.g.lymph, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:127 as residues: Pro-32 to Gly-39.

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The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in breast lymph nodes indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these 20 sequences are related to SEQ ID NO:39 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence 25 described by the general formula of a-b, where a is any integer between 1 to 911 of SEQ ID NO:39, b is an integer of 15 to 925, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where the b is greater than or equal to a + 14.

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#### FEATURES OF PROTEIN ENCODED BY GENE NO: 30

The translation product of this gene was shown to have homology to the unc-50 related protein of Rattus norvegicus (See Genebank Accession No. gil2735550) which is thought to be a novel RNA-binding protein that regulates neuronal nicotinic receptor expression. Preferred polypeptides comprise the following amino acid sequence: QDSRKMLPSTSVNSLVQGNG

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VLNSRDAARHTAGAKRYKYLRRLFRFRQMDF

EFAAWQMLYLFTSPQRVYRNFHYRKQTKDQWARDDPAFLVLLSIWLCV

STI GFGFVLD (SEQ ID NO:207) NXQSRDYDVEWGYAFDVHLNAFYPLLV

ILHFIQLFFINHVILTDTFIGYLVGNTLWLVAVGYYIYVTFLGYSALPFLKNT

VIL LYPFAPLILLYGLSLALGWNFTHTLCSFYKYRVK (SEQ ID NO:208),

SVNS LVQGNGVLNSRDAARHTAGAKRYKYLRRLFRFRQMDFEFAA (SEQ ID NO:209), VILTDTFIGYLVGNTLWLVAVGY (SEQ ID NO:210), and/or

GWNFT HTLCSFYKYRV (SEQ ID NO:211). Also preferred are the

polynucleotides encoding these polypeptides.

This gene is expressed primarily in hematopoietic tissues and to a lesser extent in prostate, placenta, and other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, neural, and inflammatory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, immune, cancerous, or wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution combined with the homology to a putative, brain-specific transcription factor indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system

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disorders. Expression of this gene product in hematopoeitic tissue indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the genc is expressed in cells 5 of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or 10 immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for 15 the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:40 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related 20 sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1205 of SEQ ID NO:40, b is an integer of 15 to 1219, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where the b is 25 greater than or equal to a + 14.

# 30 FEATURES OF PROTEIN ENCODED BY GENE NO: 31

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This gene is expressed primarily in proliferating tissues and tumors, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, growth related diseases and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological

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probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of tumors such as breast cancer, colon cancer, and many other common cancers expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.differentiating, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within tumor tissues and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. In such an event, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoietic lineages from early hematopoietic stem and committed progenitor cells. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:41 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related 25 sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1710 of SEQ ID NO:41, b is an integer of 15 to 1724, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where the b is 30 greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 32 35

This gene is expressed primarily in placenta, lung, and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental, reproductive, and pulmonary disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the lung and placenta, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.reproductive, pulmonary, or cancerous and wounded tissues) or bodily fluids (e.g.pulmonary surfactant, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another 10 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:130 as residues: Met-1 to Trp-7, Ala-15

37 to Arg-48. The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of developmental and pulmonary disorders, particularly of cancer since development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:42 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 784 of SEQ ID NO:42, b is an integer of 15 to 798, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where the b is greater than or equal to a + 14.

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#### FEATURES OF PROTEIN ENCODED BY GENE NO: 33

The translation product of this gene was shown to have homology to the human mitosis-associated nuclear antigen RMSA-1 which may be useful as an antisense therapy for blocking the onset of mitosis (See Genebank Accession No.O72501).

This gene is expressed primarily in spleen of chronic lymphocytic leukemia.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoetic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and hematopoetic, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in leukemia cells combined with its homology to a mitotic regulatory factor indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or

proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:43 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 679 of SEQ ID NO:43, b is an integer of 15 to 693, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where the b is greater than or equal to a + 14.

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 34

The sequence of this gene was shown to have homology to the guinea pig platelet activating factor (PAF) receptor which is a unique phospholipid mediator, possesses potent proinflammatory, smooth-muscle contractile and hypotensive activities, and appears to be crucial in the pathogenesis of bronchial asthma and in the lethality of endotoxin and anaphylactic shock. Sequence analysis indicates that the receptor belongs to the superfamily of G protein-coupled receptors. (See Genebank Accession No.gblX56736lCCPAFREC).

This gene is expressed primarily in human brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders related to central nervous system, as well as the hematopoetic system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, hematopeotic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid

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from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:132 as residues: Pro-25 to Thr-31.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Considering the homoology to a platelet activating factor, in addition the tissue distribution in brain, indicates that the protein product of this gene may show utility in the diagnosis, treatment, and/or prevention of stroke, amnesia, and other neural disorders related to vascular trauma and inflammation. Protein, as well as, antibodies directed against the protein may 15 show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:44 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically 20 excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1344 of SEQ ID NO:44, b is an integer of 15 to 1358, where both a and b correspond to the positions of nucleotide 25 residues shown in SEQ ID NO:44, and where the b is greater than or equal to a + 14.

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 35

This gene is expressed primarily in primary dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, skin disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential

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identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the epithelial cells of skin, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.integumentary, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:133 as residues: His-106 to Ser-117.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowenís disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Pagetís disease, mycosis fungoides, and Kaposiís sarcoma), injuries and inflammation of the skin (i.e.wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, althletes foot, and ringworm). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:45 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 951 of SEQ ID NO:45, b is an integer of 15 to 965, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where the b is greater than or equal to a + 14. 35

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### FEATURES OF PROTEIN ENCODED BY GENE NO: 36

This gene is expressed primarily in macrophages.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoetic, and/or immune disorders and afflictions, particularly bacterial infections. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above 10 tissues or cells, particularly of the immunesystem, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and hematopoetic, immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, 15 relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:134 as residues: Ser-12 to Trp-19, Val-51 to Thr-57, Ser-103 to Glu-116, His-123 to Leu-130, Gln-138 to Gly-143. 20

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against

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the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:46 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 777 of SEQ ID NO:46, b is an integer of 15 to 791, where both a and b correspond to the 10 positions of nucleotide residues shown in SEQ ID NO:46, and where the b is greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 37 15

This gene is expressed primarily in human microvascular endothelial cells. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, vascular diseases, particularly stroke. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the blood vescle system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.vascular, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, and/or prevention of vascular diseases, such as vasculitis, varicose veins, stroke, aneurysm, in addition to disorders involving vasodilation and constriction. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:47 and may have

been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 756 of SEQ ID NO:47, b is an integer of 15 to 770, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where the b is greater than or equal to a + 14.

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### FEATURES OF PROTEIN ENCODED BY GENE NO: 38

This gene is expressed primarily in human rhabdomyosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuromuscular disorders, particularly cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.muscle, neural, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:136 as residues: Ser-82 to Val-87, Pro-103 to Gly-110.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various muscle disorders, such as muscular dystrophy, cardiomyopathy, fibroids, myomas, and rhabdomyosarcomas. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:48 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present

invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 861 of SEQ ID NO:48, b is an integer of 15 to 875, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where the b is greater than or equal to a + 14.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 39

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This gene is expressed primarily in spleen metastatic melanoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoetic, and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoeitic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.hematopoetic, immune, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:137 as residues: Met-1 to Lys-7.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well

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as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:49 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 600 of SEQ ID NO:49, b is an integer of 15 to 614, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:49, and where the b is greater than or equal to a + 14.

# 20 FEATURES OF PROTEIN ENCODED BY GENE NO: 40

The translation product of this gene was shown to have homology to a zinc finger protein of Rattus norvegicus which is known to be testis-specific and, as such, may suggest that the protein would have utility as a transcription factor (See Genebank Accession No. gil57504). One embodiment of this gene comprises polypeptides of the following amino acid sequence:

PMVLKLKDWPPGEDFRDMMP (SEQ ID NO:212), YFVRPDLGPKMYNAYG

PMVLKLKDWPPGEDFRDMMP (SEQ ID NO:212), YFVRPDLGPKMYNAYG (SEQ ID NO:213), NSAREDGQP (SEQ ID NO:214), and/or LNLASRLP (SEQ ID NO:215). An additional embodiment is the polynucleotides encoding these polypeptides.

This gene is expressed primarily in bone marrow cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and hematopoetic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.hematopoetic, immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

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The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of 10 cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may 15 have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, based upon the homology to a testis-specific zinc finger protein may suggest that the protein product of this gene is useful in the diagnosis, treatment, and/or prevention of various male reproductive disorders. Protein, as 20 well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:50 and may have been publicly available prior to conception of the present invention. 25 Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 542 of SEQ ID NO:50, b is an integer of 15 to 556, 30 where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:50, and where the b is greater than or equal to a + 14.

### 35 FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene is expressed primarily in bone marrow cells.

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Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, obesity and bone marrow disorders, particularly of the hematopoetic system. Similarly, polypeptides and antibodies directed to these 5 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.hematopoetic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, 10 serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:139 as residues: Arg-52 to Asn-60, 15 Asn-65 to Ala-73, Ala-81 to Ser-89.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:51 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 989 of SEQ ID NO:51, b is an integer of

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15 to 1003, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where the b is greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 42 5

This gene is expressed primarily in teratocarcinoma cells, and to a lesser extent in human amygdala.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neural disorders, particularly cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain or CNS, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:140 as residues: Pro-20 to Cys-26. 20

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, preception, and particularly cancer. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:52 and may have been publicly available prior to conception of the present invention. 35 Preferably, such related polynucleotides are specifically excluded from the scope of

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the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 872 of SEQ ID NO:52, b is an integer of 15 to 886, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:52, and where the b is greater than or equal to a + 14.

# FEATURES OF PROTEIN ENCODED BY GENE NO: 43

When tested against promyelocyctic cell lines, supernatants removed from cells containing this gene activated the GAS (gamma activation site) pathway. Thus, it is likely that this gene activates mycloid cells through the Jaks-STAT signal transduction pathway GAS is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in human neutrophil.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoetic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoetic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:141 as residues: Gly-11 to Ser-18, Thr-26 to Lys-36.

The tissue distribution combined with the biological activity within myeloid cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders.

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Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, 10 antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against 15 the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:53 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are 20 specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 550 of SEQ ID NO:53, b is an integer of 15 to 564, where both a and b correspond to the 25 positions of nucleotide residues shown in SEQ ID NO:53, and where the b is greater than or equal to a + 14.

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#### FEATURES OF PROTEIN ENCODED BY GENE NO: 44 30

This gene is expressed primarily in human neutrophil.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoetic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of

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disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:142 as residues: Leu-41 to Glu-48.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:54 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 919 of 35 SEQ ID NO:54, b is an integer of 15 to 933, where both a and b correspond to the

positions of nucleotide residues shown in SEQ ID NO:54, and where the b is greater than or equal to a + 14.

# 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 45

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When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon-sensitive responsive element). Thus, it is likely that this gene activates kidney and endothelial cells through the Jaks-STAT signal transduction pathway. ISRE is also a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and hematopoetic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the disorders relating to hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:143 as residues: Met-1 to His-6, Cys-29 to Ser-49, Pro-72 to Gly-77.

The tissue distribution combined with the biological activity in stimulating the interferon-sensitive responsive element indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages,

including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:55 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 583 of SEQ ID NO:55, b is an integer of 15 to 597, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:55, and where the b is greater than or equal to a + 14.

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#### FEATURES OF PROTEIN ENCODED BY GENE NO: 46

The translation product of this gene was shown to have homology to the human thromboxane A2 receptor which is known to be a potent stimulator of platelet aggregation (See Genebank Accession No. P21731). This gene maps to chromosome 19, and therefore, may be used as a marker in linkage analysis for chromosome 19.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neutropenia and neutrophia, and other immunological and

hematopoetic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases relating to hemopoietic system,

5 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene 15 product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including 20 arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and 25 committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these 30 sequences are related to SEQ ID NO:56 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence 35 described by the general formula of a-b, where a is any integer between 1 to 759 of SEQ ID NO:56, b is an integer of 15 to 773, where both a and b correspond to the

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positions of nucleotide residues shown in SEQ ID NO:56, and where the b is greater than or equal to a+14.

### 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 47

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions:neutropenia and other hemopoetic or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the disorders relating to hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and hemopoetic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:145 as residues: Pro-14 to Pro-28.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or

proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:57 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 719 of SEQ ID NO:57, b is an integer of 15 to 733, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where the b is greater than or equal to a + 14.

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#### FEATURES OF PROTEIN ENCODED BY GENE NO: 48

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neutropenia, and other hemopoetic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases relating to hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:146 as residues: Pro-23 to Tyr-28.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene

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product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions.

of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:58 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present

sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 517 of SEQ ID NO:58, b is an integer of 15 to 531, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58, and where the b is greater than or equal to a + 14.

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#### FEATURES OF PROTEIN ENCODED BY GENE NO: 49

The translation product of this gene was shown to have homology to the human cathepsin E which is thought to play a role in modulation of the immune system (See Genebank Accession No.P14091). This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hemopoetic or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological

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probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution combined with its homology to a conserved human cathepsin gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:59 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 838 of 35 SEQ ID NO:59, b is an integer of 15 to 852, where both a and b correspond to the

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positions of nucleotide residues shown in SEQ ID NO:59, and where the b is greater than or equal to a + 14.

# 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 50

The translation product of this gene was shown to have homology to the human uridine 5' monophosphate synthase which is known to be involved in purine biosynthesis (See Genebank Accession No. P11172). This gene maps to chromosome 3, and therefore, may be used as a marker in linkage analysis for chromosome 3.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hemopoetic or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hemopoetic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or

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immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences. are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:60 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 666 of SEQ ID NO:60, b is an integer of 15 to 680, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60, and where the b is 15 greater than or equal to a + 14.

## FEATURES OF PROTEIN ENCODED BY GENE NO: 51

This gene is expressed primarily in neutrophils.

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Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurotropenia, and other hemopoetic or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:149 as residues: Gln-73 to Gln-82.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of

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hematopoetic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility 10 as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:61 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from 15 the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 880 of SEQ ID NO:61, b is an integer of 15 to 894, where both a and b correspond to the positions of nucleotide residues 20 shown in SEQ ID NO:61, and where the b is greater than or equal to a + 14.

## FEATURES OF PROTEIN ENCODED BY GENE NO: 52

The translation product of this gene was shown to have homology to the 25 enhancer-trap-locus-1 of Mus musculus (See Genebank Accession No. gil50866) which is thought to be involved in gene regulation pathways during mouse development, particularly in the regulation of homeotic genes. As such, it can be suggested that the protein product of this gene would play a similiar role in humans. 30

One embodiment of this gene comprises polypeptides of the following amino acid sequence:

VKPDPPRAPGENEDSSVPETPDNERKASISYFKNQRGIQYIDLSSDSEDVVSP N

CSNTVQEKTFNKDTVIIVSEPSEDEESQGLPTMARRNDDISELEDLSELEDLK DAKLQTLKELFPQRSDN DLLKVIFIGYCSCNDDKISPAFSAIVSSG (SEQ ID 35 NO:216), KDAKLQTLKELFPQRSD (SEQ ID NO:217), KDTVIIVSEPSEDEES

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(SEQ ID NO:218), and/or EDSSVPETPDNERKAS (SEQ ID NO.219). An additional embodiment is the polynucleotides encoding these polypeptides.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions:hemopoietic or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:150 as residues: Lys-38 to Gln-46.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, considering the homology to a conserved homeobox protein, would suggest that the protein product of this gene is useful in the detection, treatment, and/or prevention of developmental disorders, particularly those involving the immune system (e.g. immunodeficiencies secondary PCT/US98/15949 WO 99/06423

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to congentital defects or loss of immune organs). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:62 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 677 of SEQ ID NO:62, b is an integer of 15 to 691, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62, and where the b is greater than or equal to a + 14.

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 53

When tested against PC12 cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) pathway. Thus, it is likely that this gene activates sensory neuron cells through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jaks-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation.

This gene is expressed primarily in human B cell lymphoma and neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders, particularly of B cell related diseases, and disorders related to hemopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, hemopoietic, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the

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standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:151 as residues: Met-1 to Asp-12.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates 5 a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. Considering the expression in B-cell lymphomas, this gene product may be involved in the regulation of cytokine production, antigen presentation, or other 10 processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, lymphomas, acne, and psoriasis. Protein, as 15 well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against 20 the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:63 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are 25 specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 877 of SEQ ID NO:63, b is an integer of 15 to 891, where both a and b correspond to the 30 positions of nucleotide residues shown in SEQ ID NO:63, and where the b is greater than or equal to a + 14.

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This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neutropenia, and other hemopoietic or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown 15 in SEQ ID NO:152 as residues: Ser-32 to Cys-37.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:64 and may have been publicly available prior

to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 944 of SEQ ID NO:64, b is an integer of 15 to 958, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where the b is greater than or equal to a + 14.

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### FEATURES OF PROTEIN ENCODED BY GENE NO: 55

When tested against PC12 cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) pathway. Thus, it is likely that this gene activates sensory neuron cells through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jaks-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions:neutropenia, and other immune or hemopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, hemopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene

product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions.

Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these

are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:65 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 788 of SEQ ID NO:65, b is an integer of 15 to 802, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:65, and where the b is

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 56

This gene is expressed primarily in fetal liver.

greater than or equal to a + 14.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hepatoblastoma, hepatitis, liver metabolic diseases, and conditions that are attributable to the differentiation of hepatocyte progenitor cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the liver, expression of this gene at significantly higher or lower levels may be routinely

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detected in certain tissues (e.g.hepatic, developing, or cancerous and wounded tissues) or bodily fluids (e.g.bile, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:154 as residues: His-27 to Arg-34.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). In addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various would-healing models and/or tissue trauma. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:66 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1078 of SEQ ID NO:66, b is an integer of 15 to 1092, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:66, 25 and where the b is greater than or equal to a + 14.

## FEATURES OF PROTEIN ENCODED BY GENE NO: 57

This gene is expressed primarily in IL-1 and LPS induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neutropenia, and other immune or hemopoietic disorders, particularly bacterial infections. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above

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tissues or cells, particularly of the diseases relating to hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for 25 the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:67 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related 30 sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 720 of SEQ ID NO:67, b is an integer of 15 to 734, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:67, and where the b is 35 greater than or equal to a + 14.

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## FEATURES OF PROTEIN ENCODED BY GENE NO: 58

This gene is expressed primarily in IL-1 and LPS induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neutropenia, and other hemopoietic or immune disorders, particularly bacterial infections. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the disorders relating to hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences,

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are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:68 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 692 of SEQ ID NO:68, b is an integer of 15 to 706, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:68, and where the b is greater than or equal to a + 14. 10

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 59 This gene is expressed primarily in IL-1 and LSP induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, infection, inflammation, in addition to disorders of the immune or hemopoietic systems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at

significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions.

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Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences. are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:69 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 422 of SEQ ID NO:69, b is an integer of 15 to 436, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:69, and where the b is greater than or equal to a + 14.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 60

This gene is expressed primarily in IL-1 and LSP treated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bacterial infections, inflammation, in addition to disorders of the hemopoietic or immune systems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the

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standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for 20 the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:70 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related 25 sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 707 of SEQ ID NO:70, b is an integer of 15 to 721, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:70, and where the b is 30 greater than or equal to a + 14.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 61

This gene is expressed primarily in IL-1 and LSP treated neutrophils. 35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

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biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bacterial infection, inflammation, in addition to disorders of the hemopoietic or immune systems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissuc(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:159 as residues: Glu-36 to Lys-46.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:71 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are 35 specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present

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invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 779 of SEQ ID NO:71, b is an integer of 15 to 793, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where the b is greater than or equal to a + 14.

## FEATURES OF PROTEIN ENCODED BY GENE NO: 62

This gene is expressed primarily in IL-1 and LSP treated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bacterial infection, inflammation, in addition to immune or hemopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:160 as residues: Gly-18 to Lys-29, Pro-45 to Gly-51, Pro-53 to Lys-58, Pro-72 to Gly-79, Pro-88 to Leu-108, Ala-25 124 to Ser-134, Ser-138 to Lys-148.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid

arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:72 and may have been publicly available prior 10 to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 747 of SEQ ID NO:72, b is an integer of 15 to 761, where both a and b correspond to the 15 positions of nucleotide residues shown in SEQ ID NO:72, and where the b is greater than or equal to a + 14.

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## FEATURES OF PROTEIN ENCODED BY GENE NO: 63

This gene is expressed primarily in IL-1 and LSP treated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune or hemopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:161 as residues: Asp-6 to Glu-15, Pro-76 to Ser-87.

88 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or 15 proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:73 and may have been publicly available prior 20

to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 659 of SEQ ID NO:73, b is an integer of 15 to 673, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:73, and where the b is greater than or equal to a + 14.

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 64

This gene is expressed primarily in IL-1 and LSP treated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune or hemopoietic disorders. Similarly, polypeptides and

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antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against 25 the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:74 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are 30 specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 569 of SEQ ID NO:74, b is an integer of 15 to 583, where both a and b correspond to the 35

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positions of nucleotide residues shown in SEQ ID NO:74, and where the b is greater than or equal to a + 14.

### 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene maps to chromosome 19, and therefore, may be used as a marker in linkage analysis for chromosome 19.

This gene is expressed primarily in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, Inflammatory bowel disease, chronic neutropenia (Kostmann's syndrome), chemotherapy induced neutropenia, AIDS, and other immunodefiencicy disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:163 as residues: Gly-17 to Gly-23.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or

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immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:75 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 787 of SEQ ID NO:75, b is an integer of 15 to 801, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where the b is 15 greater than or equal to a + 14.

# FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This gene is expressed primarily in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, chronic and acute neutropenia, inflammatory bowel disease, neutrophil related multiple organ failure, and other immune or hemopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and hemopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:164 as residues: Met-35 to Glu-51.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid 10 arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or 15 proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:76 and may have been publicly available prior 20 to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 968 of 25 SEQ ID NO:76, b is an integer of 15 to 982, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76, and where the b is greater than or equal to a + 14.

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 67

This gene is expressed primarily in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, acute and chronic neutropenia, inflammatory bowel disease,

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neutrophil-related multiple organ failure, and other immune or hemopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and hemopoietic, or cancerous and wounded tissues) or bodily fluids (c.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:165 as residues: Asp-21 to His-26, Leu-31 to His-39, Arg-64 to Thr-70.

The tissue distribution of this gene specifically in neutrophils indicates a possible role in the treatment and/or detection of disease states in which either a lack or excess of neutrophils plays a role in the pathophysiology of the disease state. Targetting this protein could provide a mechanism to inhibit the role of neutrophils in Inflammatory bowel disease and neutrophil releted multiple organ failure. The protein encoded by this gene could be important in the treatment of neutropenia, such as the chronic neutropenic Kostmann's syndronme, AIDS related neutropenia, chemotherapy induced neutropenia, in addition to juvenile periodontis and other states which are caused by decreased neutrophil chemotaxis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:77 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 987 of SEQ ID NO:77, b is an integer of 15 to 1001, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where the b is greater than or equal to a + 14.

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## FEATURES OF PROTEIN ENCODED BY GENE NO: 68

This gene is expressed primarily in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neutropenia, inflammatory bowel disease, neutrophil related multiple organ failure, and other immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and hemopoietic, cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:166 as residues: Ile-26 to Ala-34, Thr-81 to Asp-88.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences,

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are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:78 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 734 of SEQ ID NO.78, b is an integer of 15 to 748, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where the b is greater than or equal to a + 14.

# FEATURES OF PROTEIN ENCODED BY GENE NO: 69

This gene is expressed primarily in adipocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, obesity, and diabetes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.endocrine, metabolic, or cancerous and wounded tissues) or bodily fluids (e.g. serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:167 as residues: Ser-26 to Lys-36.

The tissue distribution predominantly in adipose tissue, indicates a role in the treatment and/or detection of adipofibrosarcoma, adiponecrosis, obesity and diabetes. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:79 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

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Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 572 of SEQ ID NO:79, b is an integer of 15 to 586, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:79, and where the b is greater than or equal to a + 14.

# FEATURES OF PROTEIN ENCODED BY GENE NO: 70

This gene is expressed primarily in kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, kidney diseases, particularly nephritis and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal and urogenital systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.urogenital, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritus, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:80 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide

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sequence described by the general formula of a-b, where a is any integer between 1 to 532 of SEQ ID NO:80, b is an integer of 15 to 546, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:80, and where the b is greater than or equal to a + 14.

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 71

This gene is expressed primarily in T-cells and hepatocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and hepatic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hepatic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, hepatic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and

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committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, considering the expression in hepatocytes indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are 5 attributable to the differentiation of hepatocyte progenitor cells). In addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various would-healing models and/or tissue trauma. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST 10 sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:81 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded 15 from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 694 of SEQ ID NO:81, b is an integer of 15 to 708, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:81, and 20 where the b is greater than or equal to a + 14.

## FEATURES OF PROTEIN ENCODED BY GENE NO: 72

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The translation product of this gene was shown to have homology to the human KIAA0213 which is thought to be a serine/threonine protein kinase which may implicate this gene as playing an integral role in signal transduction, particularly in cell cycle regulation (See Genebank Accession No. P25390). When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon-sensitive responsive element ) pathway. Thus, it is likely that this gene activates kidney cells through the Jak-Stat signal transduction pathway. ISRE is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

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This gene is expressed primarily in rhabdomyosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, rhabdomyosarcoma, and other cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.proliferating, muscle, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:170 as 15 residues: Ser-24 to Ala-30.

The tissue distribution in rhabdomyosarcoma tissue combined with its homology to a putative cell cycle modulating protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders, particularly of muscle tissue. Expression within tumor tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Alternatively, considering its expression in muscle tissue may suggest indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various muscle disorders, such as muscular dystrophy, cardiomyopathy, fibroids, myomas, and rhabdomyosarcomas. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:82 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 810 of SEQ ID NO:82, b is an integer of

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15 to 824, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:82, and where the b is greater than or equal to a + 14.

# 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 73

When tested against fibroblast cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1 pathway. Thus, it is likely that this gene activates cells through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jaks-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation.

This gene is expressed primarily in T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders and disease states. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well

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as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:83 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related 10 sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 775 of SEQ ID NO:83, b is an integer of 15 to 789, where both a and b correspond to the 15 positions of nucleotide residues shown in SEQ ID NO:83, and where the b is greater than or equal to a + 14.

# 20 FEATURES OF PROTEIN ENCODED BY GENE NO: 74

The translation product of this gene was shown to have homology to the human zinc finger protein 7 which is thought to a play a role as a transcriptional modulator (See Genebank Accesion No. P17097). This gene maps to the chromosome X, and therefore, may be used as a marker in linkage analysis for the chromosome X.

This gene is expressed primarily in T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders and disease states. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having

such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:172 as residues: Glu-4 to Arg-12, Glu-63 to Arg-69.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment 10 of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well 15 as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against 20 the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:84 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are 25 specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 797 of SEQ ID NO:84, b is an integer of 15 to 811, where both a and b correspond to the 30 positions of nucleotide residues shown in SEQ ID NO:84, and where the b is greater than or equal to a + 14.

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This gene is expressed primarily in anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemias, lymphomas, auto-immunities, immunodeficiencies, immuno-supressive conditions and hematopoeitic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoeitic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-supressive conditions (transplantation) and hematopoeitic disorders. In addition this gene product may be applicable in conditions of general microbial infection, inflammation or cancer. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:85 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1056 of SEQ ID NO:85, b is an integer of 15 to 1070, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:85, and where the b is greater than or equal to a + 14.

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## FEATURES OF PROTEIN ENCODED BY GENE NO: 76

This gene maps to chromosome 11, and therefore, may be used as a marker in linkage analysis for chromosome 11.

This gene is expressed primarily in T-cells (resting and anergic).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemias, lymphomas, auto-immunities, immunodeficiencies, immuno-supressive conditions and hematopoeitic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoeitic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:174 as residues: Thr-25 to Asp-38.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-supressive conditions (transplantation) and hematopoeitic disorders. In addition this gene product may be applicable in conditions of general microbial infection, inflammation or cancer. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:86 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 713 of SEQ ID NO:86, b is an integer of 15 to 727, where both a and b

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correspond to the positions of nucleotide residues shown in SEQ ID NO:86, and where the b is greater than or equal to a + 14.

## 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 77

This gene maps to chromosome 8, and therefore, may be used as a marker in linkage analysis for chromosome 8.

This gene is expressed primarily in anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemias, lymphomas, auto-immunities, immunodeficiencies, immuno-supressive conditions and hematopoeitic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoeitic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:175 as residues: Glu-8 to Lys-17, Val-42 to Trp-51.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-supressive conditions (transplantation) and hematopoeitic disorders. In addition this gene product may be applicable in conditions of general microbial infection, inflammation or cancer. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:87 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded

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from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 676 of SEQ ID NO:87, b is an integer of 15 to 690, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:87, and where the b is greater than or equal to a+14.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 78

This gene is expressed primarily in anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemias, lymphomas, auto-immunities, immunodeficiencies, immuno-supressive conditions and hematopoeitic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoeitic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. blood cells, and immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-supressive conditions (transplantation) and hematopoeitic disorders. In addition this gene product may be applicable in conditions of general microbial infection, inflammation or cancer. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:88 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded

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from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 882 of SEQ ID NO:88, b is an integer of 15 to 896, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:88, and where the b is greater than or equal to a+14.

# FEATURES OF PROTEIN ENCODED BY GENE NO: 79

The translation product of this gene was shown to have homology to the human clathrin light chain B which is the major protein for the polyhedral coat of clathrin coated pits and vesicles (See Genebank Accession No. P09497).

This gene is expressed primarily in the spinal cord.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, meningitis, spina bifida, spinal tumors and neoplasms as well as other developmental and neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the spinal cord and central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, or cancerous and wounded tissues) or bodily fluids (e.g.serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in spinal cord combined with the homology to human clathrin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of trauma, meningitis, spina bifida, spinal tumors and neoplasms as well as other developmental and neurodegenerative conditions of the spinal cord and central nervous system, particularly those neural disorders involving cell-cell signalling. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:89 and may have been publicly available prior to conception of the present invention. Preferably, such related

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polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 843 of SEQ ID NO:89, b is an integer of 15 to 857, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:89, and where the b is greater than or equal to a + 14.

# 10 FEATURES OF PROTEIN ENCODED BY GENE NO: 80

This gene is expressed primarily in spinal cord.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, meningitis, spina bifida, spinal tumors and neoplasms as well as other developmental and neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the spinal cord and central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, or cancerous and wounded tissues) or bodily fluids (e.g. serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of trauma, meningitis, spina bifida, spinal tumors and neoplasms as well as other developmental and neurodegenerative conditions of the spinal cord and central nervous system, such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are

related to SEQ ID NO:90 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 547 of SEQ ID NO:90, b is an integer of 15 to 561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:90, and where the b is greater than or equal to a + 14.

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## FEATURES OF PROTEIN ENCODED BY GENE NO: 81

This gene is expressed primarily in spinal cord.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, meningitis, spina bifida, spinal tumors and neoplasms as well as other developmental and neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the spinal cord and central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, or cancerous and wounded tissues) or bodily fluids (e.g. serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:179 as residues: Met-1 to Arg-6, Ser-98 to Met-104.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of trauma, meningitis, spina bifida, spinal tumors and neoplasms as well as other developmental and neurodegenerative conditions of the spinal cord and central nervous system, such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns,

balance, and preception. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:91 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 641 of SEQ ID NO:91, b is an integer of 15 to 655, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:91, and where the b is greater than or equal to a + 14.

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# FEATURES OF PROTEIN ENCODED BY GENE NO: 82

This gene is expressed primarily in spinal cord.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, meningitis, spina bifida, spinal tumors and neoplasms as well as other developmental and neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the spinal cord and central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.neural, or cancerous and wounded tissues) or bodily fluids (e.g. serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:180 as residues: Asn-9 to Tyr-14, Ala-30 to Val-39.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of trauma, meningitis, spina bifida, spinal tumors and neoplasms as well as other developmental and neurodegenerative conditions of the spinal cord and central

nervous system, such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. Protein, as well as, antibodies directed against the protein 5 may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:92 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically 10 excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 834 of SEQ ID NO:92, b is an integer of 15 to 848, where both a and b correspond to the positions of nucleotide 15 residues shown in SEQ ID NO:92, and where the b is greater than or equal to a +

# 20 FEATURES OF PROTEIN ENCODED BY GENE NO: 83

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This gene is expressed primarily in fibrosarcoma, and tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, fibrosarcoma, tosilitis, and other muscle or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and musculoskeletal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.immune, muscle, or cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of

PCT/US98/15949 WO 99/06423

immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment 5 of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. Protein, as well 10 as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, the expression in fibrosarcoma 15 indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various muscle disorders, such as muscular dystrophy, cardiomyopathy, fibroids, myomas, and rhabdomyosarcomas. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above 20 listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:93 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is 25 cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 598 of SEQ ID NO:93, b is an integer of 15 to 612, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:93, and where the b is greater than or equal to a + 30 14.

TABLE

|                        | St.                           | -/·         |                   | Ц                 | ; J <sub>v</sub> | <u>-</u> -      |            | 11.      |            | 30        | ·                 | 000      | 2                 | 113      |                   | 131       |                   |           |
|------------------------|-------------------------------|-------------|-------------------|-------------------|------------------|-----------------|------------|----------|------------|-----------|-------------------|----------|-------------------|----------|-------------------|-----------|-------------------|-----------|
|                        | La                            | Ą           | Jo                | _                 |                  | G<br>—          |            | 1        |            | 1         | ,                 | 1        | 1                 | +        |                   | +         |                   | $\dashv$  |
|                        | irst AA                       | of          | Sig Secreted      | Dortion           | romon I          | 31              |            | 40       | P<br>F     | 77        | ì                 | 7)       | 1                 | 104      |                   | 26        | i<br>i            |           |
| ast                    | AA<br>F                       | Jo          | C. C.             | 2 in              | $\neg \tau$      | 30              |            | 30       |            | 75        | 07                | 5        | 7                 | 30       | <u>`</u>          | 25        | í                 |           |
| irst                   | ₹                             | of          |                   | 318               | d b              |                 |            | -        | -          | -         | _                 | -        | _                 | -        | -                 | -         | -                 |           |
|                        | EQ /                          |             | <u> </u>          | <u></u>           |                  | <del> </del> 66 |            |          | <u> </u>   |           | 101               | (        | 701               | 103      | 501               | 101       | 101               |           |
| 5: NT of AA First Last | First SEO AA AA First AA Last | AA of ID of |                   | Start Signal INC: | Pep              | 1072            |            | $\dashv$ | 566        |           | 503               |          | 157               | 5,50     | 942               |           | 1230              |           |
|                        | ry.                           |             | 5 ,               | Start             | Codon Pep        | 1072            | _          |          | 995        |           | 503               |          | 157               |          | 947               |           | 1720              |           |
| TN.                    | , to                          | ·           | 21017             | Sed.              | <u> </u>         | 1761            |            |          | 1519       |           | 1071              |          | 955               | 1        | 1508              |           | 2006              |           |
| c, NT 3, NT            | C 1 V 5                       | 7 2         | Total Cione Cione | Sed.              |                  | 952             | _          |          | 606        |           | 483               |          | 65                |          | 847               |           | 16 2006 1225 2006 |           |
| <u> </u>               | <u> </u>                      |             | lotal             | K                 | Seq.             | 1761            |            |          | 1519       |           | 1071              |          | 955               |          | 1508              |           | 2006              |           |
| ļ                      | - (Z                          | ZHZ<br>ZHZ  | <u> </u>          | SO.               | ×                | F               |            |          | 12         |           | 13                |          | 14                |          | 15                |           |                   |           |
|                        |                               |             |                   |                   | Vector           |                 | UNI-CAF AN |          | Lambda ZAP | П         | 209145 Uni-ZAP XR |          | 209145 Uni-ZAP XR |          | 209145 Uni-ZAP XR |           | Uni-ZAP XR        |           |
|                        |                               | ATCC        | Deposit           | Nr and            | Date             |                 | 209145     | 16/11/10 | 209145     | 07/11/197 | 209145            | 76/11/10 | 209145            | 16/11/10 | 209145            | 07/11/197 | 209148            | 07/11/197 |
|                        |                               |             |                   | cDNA              | Clone ID         |                 | HTECE94    |          | HTWAH05    |           | HAQAN31           | ,        | HAUAQ39           |          | HBNAU27           |           | HSIDD28           |           |
|                        |                               |             |                   | Gene              |                  | 110.            |            |          | 2          |           | 3                 |          | 4                 |          | ς,                |           | 9                 |           |

| NT   STATE   STATE |
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| NT       Seq.       Seq.       Seq.       Seq.       Codon       Pep       Y       Pep       Pep       Portion       OR         545       1       538       15       15       105       1       27       28       8         602       1       602       61       61       106       1       27       28       8         587       1       587       237       237       107       1       25       26       4         644       1       644       1       644       1       644       138       308       108       1       30       31       4         1257       142       823       823       109       1       18       19       3         541       39       541       151       151       110       1       32       33       3         557       1       567       64       64       111       1       22       23         4       586       1       586       62       62       112       1       21       21       22   |
| Seq.       Seq.       Coulon 1 of 1  |
| 54.5       1       502       61       61       106       1       27       28       6         602       1       662       61       61       106       1       27       28       6         587       1       587       237       237       107       1       25       26       4         644       1       644       1       644       1       644       1       308       308       108       1       30       31       4         1257       142       823       823       109       1       18       19       3         5       541       39       541       151       151       110       1       32       33       3         3       567       1       567       64       64       111       1       22       23         4       586       1       586       62       62       112       1       21       22   |
| 602         61         61         106         1         27         28         6           587         137         237         107         1         25         26         4           644         1         644         308         308         108         1         30         31         4           1257         142         823         823         109         1         18         19         3           541         39         541         151         151         110         1         32         33         3           3 567         1         567         64         64         111         1         22         23           4 586         1         586         62         62         62         112         1         21         22   |
| 587       1       587       237       237       107       1       25       26       4         644       1       644       308       308       108       1       30       31       4         1257       142       823       823       823       109       1       18       19         2       541       39       541       151       151       110       1       32       33         3       567       1       567       64       64       111       1       22       23         4       586       1       586       62       62       112       1       21       22  |
| 587       1       587       237       237       107       1       25       26       4         644       1       644       1       644       1       644       1       644       1       308       308       108       1       30       31       4         1257       142       823       823       823       109       1       18       19       1         541       39       541       151       151       110       1       32       33       4         557       1       567       64       64       111       1       22       23         4       586       1       586       62       62       112       1       21       22  |
| 587     1     387     237     237     308     308     108     1     30     31     4       644     1     644     308     308     108     1     30     31     4       1257     142     823     823     823     109     1     18     19       541     39     541     151     151     110     1     32     33       557     1     567     64     64     111     1     22     23       4     586     1     586     62     62     112     1     21     22  |
| 644         1         644         308         308         108         1         30         31         4           1257         142         823         823         823         109         1         18         19           541         39         541         151         151         110         1         32         33           557         1         567         64         64         111         1         22         23           4         586         1         586         62         62         112         1         21         22  |
| 644       1       644       1       644       1       644       1       2       1       1       2       1       2       1       2       1       2       1       2       1       2       1       2       1       2       1       2       1       2       1       2       1       2       1  |
| 1257     142     823     823     109     1     18     19       541     39     541     151     110     1     32     33       567     1     567     64     64     111     1     22     23       586     1     586     62     62     112     1     21     22  |
| 1257     142     823     823     825     107     1       541     39     541     151     110     1     32     33       567     1     567     64     64     111     1     22     23       586     1     586     62     62     112     1     21     22  |
| 541     39     541     151     151     110     1     32     33       567     1     567     64     64     111     1     22     23       586     1     586     62     62     112     1     21     22   |
| 541     39     541     131     131     110     1     22     23       567     11     11     1     22     23       586     1     586     62     62     112     1     21     22   |
| 567     1     567     64     64     111     1     22     23       586     1     586     62     62     112     1     21     22  |
| 567 1 567 04 04 111 1 21 22  |
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|       | Last        | AA First AA Last of of ^\lambda | Secreted | Pen Portion ( | 12 13    | ·              | 36 37 53 |                | 49 50 268   |                | 24 25 37 | i             | 17 18 121 |                | 22 23 33 |               | 54 55 178 |                | 25 45    |            |          |
|-------|-------------|---------------------------------|----------|---------------|----------|----------------|----------|----------------|-------------|----------------|----------|---------------|-----------|----------------|----------|---------------|-----------|----------------|----------|------------|----------|
| 5' NT | ¥4          | First SEQ AA                    |          |               | 1 ,      | 1134   113   1 | 138 114  |                | 1 5 1 1 5 1 |                | 711 000  | 329   110   1 | +         | 77             | 136 118  |               | 011       | 707            | 1001     |            | _        |
| (5)   |             | 5, NT                           | 10       | Seq. Start 51 | Codon    | 1510           | 130      |                |             | 12/3 150       |          | 780   329     |           | 819 22         | }        | 008   150     |           | 121/ 787       |          | 777 (9/    |          |
|       | 5' NT 3' NT | jo                              | Clone    | NT Seq. S     | Seq.     | 1510 892 1     |          | 535            |             | 1273   763     |          | 780 1         |           | 1 618          |          | 1   809       |           | 1217 395       |          | 765        |          |
|       | L           |                                 | A        | NO:           | Vector   | Uni-ZAP XR 25  |          | pBluescript 26 |             | pBluescript 27 |          | Uni-ZAP XR 28 |           | pBluescript 29 |          | Uni-ZAP XR 30 |           | pBluescript 31 | SK-      | pSport1 32 |          |
|       |             | ATCC                            | Deposit  | Nr and        | Date     | 209145 Un      | 16/11/10 | 209145 pl      | 16/11/10    | 209145 pl      | 07/17/97 | 209145        | 07/11/97  | 209145 p       | 07/11/97 | 209145        | 16/11/10  | 209145         | 16/11/10 | 209145     | 70/11/07 |
|       |             |                                 |          | cDNA          | Clone ID | HFCBD73        |          | HKIYA46        |             | HLHSA86        |          | HNGJM08       |           | HSDSB09        |          | HTGBV53       |           | H2CAA57        |          | HADFV30    |          |
|       |             |                                 |          | Gene          | Z<br>o.  | 15             |          | 91             |             | 17             |          |               |           | 19             |          | 20            |           | 21             |          | 22         |          |

| Last<br>AA<br>of<br>ORF   | 337      |            | 65         | 89         | 76         | 75         | 30               | 5                |
|---|----------|------------|------------|------------|------------|------------|------------------|------------------|
| A<br>wn   | 29       | 5          | 4<br>[     | 20         | 42         | 18         | 07               | <u>.</u>         |
|   | 28       | 95         | 40         | 61         | 41         | 17         | 61               | 4                |
| First Last AA AA of of Sig Sig Pep Pep  |          | _          | _          | _          | _          | _          |                  |                  |
| AA SEQ ID NO:   | 121      | 122        | 183        | 123        | 124        | 125        | 126              | 127              |
| 5' NT           of         AA           5' NT         AA           of         AA of         ID           Start         Signal         NO:           Codon         Pep         Y | 325      | 380        | 1480       | 37         | 589        | 406        | 154              | 59               |
| 5° NT<br>of<br>Start<br>Codon   | 325      | 380        | 1480       | 37         | 589        | 406        | 154              | 59               |
| 97  | 752      | 2192       | 2191       | 643        | 1302       | 1005       | 809              | 925              |
| 5' NT 3' NT<br>of of<br>Clone Clone<br>Seq. Seq.  | 172      | 1399       | 1398       | -          | 437        | 203        | -                |                  |
| 5'<br>Total C<br>NT Seq.  | 752      | 2265       | 2264       | 643        | 1302       | 1005       | 809              | 925              |
| SEQ X   | 33       | 34 2       | 95 2       | 35         | 36         | 37         | 38               | 39               |
| Vector  | XX       | Uni-ZAP XR | Lambda ZAP<br>II | Lambda ZAP<br>II |
| ATCC<br>Deposit<br>Nr and   | 5        |            |            | _          | 209147     |            | 209147           | 209147           |
| cDNA  |          | HAPAT76    | HAPAT76    | HLHEB47    | HLHEF54    | HLHFM06    | HLMIG41          | HLMMJ78          |
| Gene  | 23<br>23 | 24         | 24         | 25         | 56         | 27         | 28               | 29               |

| Last<br>AA<br>of<br>ORF  | 45               |                  | 70             | 34      | 32         | 117        | 145        | 4                |
|--|------------------|------------------|----------------|---------|------------|------------|------------|------------------|
| A. A   | 35               | عرد<br>و         | <del>3</del> 8 | 26      | 22         | 30         | 23         | 24               |
| Last AA F of Sig S Pep I   | 34               | 15               | 37             | 25      | 21         | 29         | 22         | 23               |
| First Last AA AA of of Sig Sig Pep Pep   | _                | _                |                |         |            | _          | _          | -                |
|  | 128              | 67.1             | 130            | 131     | 132        | 133        | 134        | 135              |
| S' NT       AA       First         First       SEQ       AA         AA of       ID       of         Signal       NO:       Sig         Pep       Y       Pep | 479              | 1254             | 262            | 28      | 564        | 327        | 118        | 141              |
| 5' NT of AA of First SEQ of AA of ID Start Signal NO: Codon Pep Y  | 479              | 1254             | 262            | 28      | 564        | 327        | 118        | 141              |
| 1 ''   |                  | 1712             | 798            | 693     | 1358       | 958        | 791        | 770              |
| S' NT 3' NT of of Clone Clone Seq. Seq.  | 429              | 1062             | -              | -       | 342        | 47         | _          | -                |
| S' NT 3' NT of of of Total Clone Clone NT Seq. Seq.  | 1219             | 1724             | 862            | 693     | 1358       | 965        | 791        | 770              |
| SEQ NO.  | 40               | 14               | 42             | 43      | 44         | 45         | 46         | 47               |
| Vector   | Lambda ZAP<br>II | Lambda ZAP<br>II | pCMVSport      | pSport1 | Uni-ZAP XR | Uni-ZAP XR | Uni-ZAP XR | Lambda ZAP<br>II |
| ATCC<br>Deposit<br>Nr and<br>Date  | 7 /6             | 1                |                | 209147  |            |            | 209147     | 209147           |
| cDNA   | 5                | HLQBR11          | HLWBZ56        | HLYBI18 | HMAJL22    | HMCAR20    | HMCAV55    | HMEFS61          |
| Gene   | 30<br>30         | 31               | 32             | 33      | 34         | 35         | 36         | 37               |

| Last<br>AA<br>of<br>ORF<br>133  | 25                 | C       | 8          | 92         | 40         | 23         | 82         | 75         |
|---|--------------------|---------|------------|------------|------------|------------|------------|------------|
| 5' NT of First Last First AA First AA AA First AA AA First AA AA First AA | 36                 | ì       |            | 33         | 24         | 21         | 20         | 36         |
| Last AA Fi of Sig S Pep F   |                    | t<br>7  |            | 32         | 23         | 20         | 19         | 35         |
| First L AA / of Sig 8   |                    | -       | _          | -          | -          |            |            | -          |
| AA First Last SEQ AA AA ID of of of NO: Sig Sig Y Pep Pep   | 100                | 13/     | 138        | 139        | 140        | 185        | 141        | 142        |
| 5' NT of  |                    | 263     | 129        | 43         | 558        | 234        | 74         | 144        |
| 5' NT of AA of D Start Signal NO: Codon Pep Y 136   | CC                 | 263     |            | 43         | 558        | 234        | 74         | 144        |
| 47  | 6/8                | 614     | 556        | 1003       | 886        | 988        | 564        | 933        |
| S' NT 3' NT of of of Total Clone Clone NT Seq. Seq.   | <u>-</u>           | 1       | -          | -          | 188        | 188        | -          | _          |
| 5<br>Total C<br>NT<br>Seq.  | 875                | 614     | 556        | 1003       | 988        | 988        | 564        | 933        |
|   | <del></del>        | 49      | 50         | 51         | 52         | 16         | 53         | 54         |
|   | Lambda ZAP<br>II   | pSport1 | Uni-Zap XR |
| ATCC<br>Deposit<br>Nr and<br>Date   | 209147<br>07/17/97 | 209147  | 209147     | 209147     | 209147     | 209147     | 209147     | 209147     |
| cDNA<br>Clone ID  | HMEJY78            | HMMAD08 | HMWFY10    | НМЖНН16    | HMWID22    | HMWID22    | HNFFC27    | HNFFC39    |
| Gene<br>No.   | 38                 | 39      | 40         | 4          | 42         | 42         | 43         | 44         |

|       |             |           |       |            | Ľ            | 7        |            | <del>.</del> |            | <u> </u> |                | <u></u>  |            | Ţ.,       |            | 33        |            | 205       |            | × ×      | ·          |          |
|-------|-------------|-----------|-------|------------|--------------|----------|------------|--------------|------------|----------|----------------|----------|------------|-----------|------------|-----------|------------|-----------|------------|----------|------------|----------|
|       |             | Last      | Ą     | of         | ORF          | 92       |            | 7            |            | 22       | _              | 30       |            | 34        | ,          | 100       |            | - -       | ·<br>      |          |            | -        |
|       |             | First AA  | of    | Secreted   | Portion      | 25       |            |              |            | <u>×</u> | )<br>•         | 40       | }<br>      | ας        | 0<br>1     | 90        | )<br> <br> | 7         | 5          | 57       | 1          |          |
|       |             | AA<br>H   | Jo    | Sig        | Pep          | 24       | I          |              |            | 17       | -              | 30       | 5.         | 27        | <u> </u>   | 35        | 1          | 7         | ) c        | V        |            |          |
|       | First Last  | AA.       | Jo    | Sig        |              | _        |            | -            | -          | -        | -              | -        |            | -         |            | -         | 4          | -         | -          | -        |            |          |
|       | AA I        | SEQ       |       |            |              | <b>-</b> | ?          | 981          | 001        | -        | 1              | 145      |            |           | 140        | 7.7.      | Ì          | -         |            | -        | 149        |          |
| S. NT | Jo          | First SEQ | AA of | Signal NO: | Pen          | 366      | 207        | 727          | 767        | C        | 25             | -        | <u>co</u>  |           | 506        |           | 7          | - 6       | 29         | r        | 46/        | _        |
|       |             | 5° NT     | Jo    |            |              | 366      | 7007       | ()           | 767        | Ç        | <del>3</del> 0 |          | 5          |           | 269        |           | 741        |           | 56         |          | 46/        |          |
|       | LN:         |           | Clone |            |              | _        | 160        | Į.           | 166        |          | 7/3            |          | 733        |           | 531        |           | 758        |           | 089        |          | 894        |          |
|       | 5' NT 3' NT | of        |       | Sed        | . <b>.</b> . | -        |            |              | _          |          |                |          | _          |           | 21         |           |            |           |            |          | -          |          |
|       |             |           | Total |            |              | Sed.     | 597        |              | 597        |          | 773            |          | 733        |           | 531        |           | 852        |           | 089        |          | 894        |          |
|       | -<br>L      | SEO       |       |            |              |          | 55         |              | 86         |          | 99             |          | 57         |           | 58         |           | 65         |           | 09         |          | 19         |          |
|       |             |           |       |            |              | Vector   | Uni-ZAP XR |              | Uni-ZAP XR |          | Uni-ZAP XR     |          | Uni-ZAP XR |           | Uni-ZAP XR |           | Uni-ZAP XR |           | Uni-ZAP XR |          | Uni-ZAP XR |          |
|       |             | ) J. V    | AICC. | Deposit    | Nr and       | Date     | 209147     |              | 209147     | 07/11/97 | 209147         | 16/11/10 | 209147     | 07/11/197 | 209147     | 07/11/197 | 209147     | 07/11/197 | 209147     | 76/11//0 | 209147     | 07/17/97 |
|       |             |           |       |            | cDNA         | Clone ID | HNGAM20    |              | HNGAM20    |          | HNGDS13        |          | HNGDS53    |           | HNGDU92    |           | HNGED06    |           | HNGEW13    |          | HNGEY51    |          |
|       |             |           |       |            | Gene         | No.      | 45         |              | 45         |          | 46             |          | 47         |           | 48         |           | 49         |           | 50         |          | 51         |          |

|       |               | st        | <b>-</b>     | <u>ب</u>         | <u>t</u>         | 9          | × ×      |              | 16       |            | _         | <u>+</u>   | -        |             | 7        |            | ,        | ~1         | ç         |            |          |
|-------|---------------|-----------|--------------|------------------|------------------|------------|----------|--------------|----------|------------|-----------|------------|----------|-------------|----------|------------|----------|------------|-----------|------------|----------|
|       |               |           | <del>\</del> |                  | $\frac{\circ}{}$ | 46         | 1        | <u> </u>     | 1        |            |           | <u> </u>   | $\dashv$ |             | -        |            | -+       |            | -         | -          | $\dashv$ |
|       |               | Ë         | ot           | Secreted         | Portion          | 47         | -        | <del>-</del> | Ç        | 70         | ,         | çç         |          | <u>`</u>    | Ç        | 3          |          |            |           | 77         |          |
|       | Last          |           | of           | Sig              | Pep              | 46         | (        | 5            | -        | 10         | (         | 32         |          | <u>ရ</u>    | G        | 77         |          |            | _         | 23         |          |
|       | AA First Last | AA.       | oť           | Sig              | Pep              | -          |          | _            |          | -          |           |            |          |             |          | -          |          |            |           |            | _        |
|       | AA<br>I       | $\sim$    |              | ÖZ               | ⊁                | 150        |          | 101          |          | 152        |           | 153        |          | 154         |          | cci        |          | 156        |           | 157        |          |
| 5. NT | of            | First SEQ | AA of ID     | Start Signal NO: | Pep              | 118        | į.       | 130          |          | 139        |           | 120        |          | 267         |          | 66<br>—    |          | 209        |           | 174        |          |
|       |               | 5. NT     | of           | Start            | Codon            | 118        |          | 136          |          | 139        |           | 120        |          | 267         |          | 66<br> -   |          | 209        |           | 174        |          |
| r     | ,<br>L        | Jo        | Jone         | Seq.             |                  | 169        |          | 891          |          | 958        |           | 802        |          | 1092        |          | 734        |          | 902        |           | 436        |          |
|       | 5' NT 3' NT   | jo        | Clone Clone  | Sed.             |                  | -          |          | 9/           |          |            |           | _          |          | 202         |          | _          |          | I          |           | _          |          |
|       |               |           | Total        |                  | Seq.             | 691        |          | 891          |          | 856        |           | 802        |          | 1092        |          | 734        |          | 902        |           | 436        |          |
| -     | LZ            | SEQ       |              | ON               |                  | 79         |          | 63           |          | 64         |           | 65         |          | 99          |          | <i>L</i> 9 |          | 89         |           | 69         |          |
|       |               |           |              | Į                | Vector           | Uni-ZAP XR |          | Uni-ZAP XR   |          | Uni-ZAP XR | -         | Uni-ZAP XR |          | pBluescript |          | Uni-ZAP XR |          | Uni-ZAP XR |           | Uni-ZAP XR |          |
|       |               | ATCC      | Denosit      | Nrand            | Date             | 7          | 07/17/97 | 209147       | 76/11/10 | 209147     | 07/11/197 | 209147     | 76/11//0 | 209148      | 76/11/10 | 209147     | 07/17/97 | 209147     | 107/11/70 | 209148     | 76/11/10 |
|       |               |           |              | ANG.             | Clone ID         | HNGEZ47    |          | HNGFQ33      |          | HNGFU38    |           | HNGIC13    |          | HSKXE22     |          | HNHBE49    |          | HNHB147    |           | HNHEC59    |          |
|       |               |           |              | 000              | Z.O.Z.           | 52         |          | 53           |          | 54         |           | 55         |          | 56          |          | 57         |          | 58         |           | 59         |          |

| 5. N.T | AA First Last | First SEQ AA AA First AA Last | AA of ID of of AA | Start Signal NO: Sig Sig Secreted of | Pep Y Pep Pep Portion ORF | 124   158   1   31   32   31 | -        | 184 159 1 29 10 10 |           | 26 160 1 15 16 138 |           | 47   161   1   30   31   89 |           | 26 162 1 61 62 04 |          | 157 163   39 40 143 |          | 29 164 1 28 29 08 |                                       | 688 165 1 55 56 89 |            |
|--------|---------------|-------------------------------|-------------------|--------------------------------------|---------------------------|------------------------------|----------|--------------------|-----------|--------------------|-----------|-----------------------------|-----------|-------------------|----------|---------------------|----------|-------------------|---------------------------------------|--------------------|------------|
| 5.     |               | 5' NT                         | Jo                |                                      |                           | 124                          |          | 184                |           | 56                 |           | 3 47                        |           | 3 26              |          | 157                 |          | 2 29              |                                       | 11 688             |            |
|        | 5' NT 3' NT   | jo jo                         | Clone Clone       | Seq. Seq.                            |                           | 30 640                       |          | 1 793              |           | 1 761              |           | 1 673                       |           | 1 583             |          | 1 801               |          | 1 985             |                                       | 1 1001             |            |
|        | LZ            | SEQ                           | ID Total          | Z                                    |                           | 70 721                       |          | 71 793             |           | 72 761             |           | 73 673                      |           | 74 583            |          | 75 801              |          | 76 982            |                                       | 77 1001            | _          |
|        |               | IS                            |                   | <u>Z</u>                             | Vector                    | (R                           |          | Uni-ZAP XR         |           | Uni-ZAP XR         |           | Uni-ZAP XR                  |           | Uni-ZAP XR        |          | Uni-ZAP XR          |          | Uni-ZAP XR        |                                       | 209148 Uni-ZAP XR  |            |
|        |               | ATCC                          | Denosit           | Nr and                               | Date                      | 209148                       | 76/11/10 | 209148             | 07/11/197 | 209148             | 07/11//97 | 209148                      | 07/11/197 | 209148            | 76/11//0 | 209148              | 76/11//0 | 209148            | 76/11//0                              | 209148             | 70/7/17/07 |
|        |               |                               |                   | PINA                                 | Clone ID                  | HNHEC63                      |          | HNHEI54            |           | HNHER77            |           | HNHES40                     |           | HNHEV43           |          | HNHFL46             |          | HNHFP80           | · · · · · · · · · · · · · · · · · · · | HNHFS63            |            |
|        |               |                               |                   | 9407                                 | Selle<br>S                | 09                           |          | 19                 |           | 62                 |           | 63                          |           | 64                |          | 65                  |          | 99                |                                       | 19                 |            |

|       |             |             |             |                  |          | _           |            |          |                   |           |           |          |            | _        |            | $\neg$   |            |          |            | Т          |            | $\neg$   |
|-------|-------------|-------------|-------------|------------------|----------|-------------|------------|----------|-------------------|-----------|-----------|----------|------------|----------|------------|----------|------------|----------|------------|------------|------------|----------|
|       |             | Last        | AA          | Jo               | ORF      | 88          | 8          | 35       | ?                 | 2,2       | -         | 36       | 0.<br>     | 57       | -,         | 177      | :<br>      | 3        |            | 25         | r<br>      |          |
|       |             | AA First AA | jo          | Secreted         | Portion  | 53          | C.C.       | 7.0      | ·1                | 30        | 06        | 7        | <u>,</u>   | 17       |            | 77       | ì          | 35       | ?;<br>     | 7.0        | ·1         |          |
| _     | Last        | AA<br>A     | of          | Sig              | Den      | رج<br>23    | 75         | ),       | 07                | 00        | 67        | ç        | )<br>      | _        | 4          | 7        | )<br>      | ,        | <u>,</u>   | - 1        | 07         | _        |
|       | First Last  | ₹           | of          | Sig              | Don      | 2           |            | -        |                   | -         | -         | -        |            | -        |            | -        | -<br>      | -        |            | <u> </u> - |            | _        |
|       | AA<br>E     |             |             |                  | _        | _           | 100        |          | 10/               |           | 891       |          | 691        |          | 0/1        | - 1      | <u></u>    | -        | 7/1        | -          | 1/3        | _        |
| Z (2) |             | First SEQ   | AA of       | Start Signal NO: | ה<br>ה   |             | 219        |          | 143               |           | 148       |          | 539        |          | 159        |          | 2/2        | -        | 23         |            | 327        |          |
| _     |             | 5° NT       | Jo          | Start            | -        | Codon       | 219        |          | 143               |           | 148       |          | 539        |          | 159        |          | 8/         |          | 23         |            | 327        |          |
|       | LN:         | of .        | Clone       | Sed              |          | $\neg \neg$ | 748        |          | 586               |           | 546       |          | 802        |          | 824        |          | 789        |          | 811        |            | 1070       |          |
|       | 5' NT 3' NT | jo          | Clone Clone | 200              | Sed.     |             |            |          | 1                 |           | -         |          | _          |          |            |          |            |          | _          |            |            |          |
|       | 4,          |             | Total       |                  | <u>-</u> | Seq.        | 748        |          | 985               |           | 546       |          | 708        |          | 824        |          | 682        |          | 811        |            | 1070       |          |
|       | E<br>Z      | CFO         |             |                  |          | ×           | 82         |          | 16                |           | 08        |          | 81         |          | 82         |          | 83         |          | 84         |            | 85         |          |
|       |             |             |             |                  |          | Vector      | Uni-ZAP XR |          | 209148 Uni-ZAP XR |           | pCMVSport | 3.0      | Uni-ZAP XR |          | Uni-ZAP XR |          | Uni-ZAP XR |          | Uni-ZAP XR |            | Uni-ZAP XR |          |
|       |             | )<br>T      | AICC        | Deposit          | Nr and   | Date        | 209148     | 07/11/97 | 209148            | 07/11//97 | 209148    | 76/11//0 | 209148     | 76/11//0 | 209148     | 76/11/10 | 209148     | 76/11/10 | 209148     | 07/11/97   | 209148     | 07/11/97 |
|       |             |             |             |                  | cDNA     | Clone ID    | HNHGC56    |          | HOUCZ78           |           | HRAAL86   |          | HRDEC77    |          | HRDEL61    |          | HSAUC38    |          | HSAUF49    |            | HSAUK57    |          |
|       |             |             |             |                  | Gene     | No.         | 89         |          | 69                |           | 70        |          | 71         |          | 72         |          | 73         |          | 74         |            | 75         |          |

| 77 7  | 64 69              | 900        |            | 52                            |            |            |                  | <del>하</del> |
|---|--------------------|------------|------------|-------------------------------|------------|------------|------------------|--------------|
| Firs<br>Sec<br>Po   | 26                 | }          | 10         | 23                            |            |            | 32               | 7            |
|   | 25                 | +          | CI         | 22                            | 25         | 46         | 31               | 13           |
| AA First Last SEQ AA AA ID of of of NO: Sig Sig Y Pep Pep   |                    | _          |            | 7                             | -<br>8     | 9          | 0                | _            |
| AA<br>SEQ<br>ID<br>NO:  | 174                |            | 176        | 177                           | 178        | 179        | 180              | 181          |
| 5' NT           of         AA         First           r NT         First         SEQ         AA           of         AA of         ID         of           Start         Signal         NO:         Sig           Codon         Pep         Y         Pep | 140                | 197        | 358        | 8                             | 351        | 46         | 191              | 147          |
| 5° NT<br>of<br>Start<br>Codon   | 140                | 197        |            | <u>∞</u>                      | 351        | 46         | 161              | 147          |
|   | 727                | 069        | 968        | 857                           | 561        | 655        | 848              | 612          |
| S' NT 3' NT of of Clone Clone Seq. Seq.   | -                  |            |            | -                             | -          | -          | 114              | _            |
| Total<br>NT<br>Seq.   | 727                | 069        | 968        | 857                           | 561        | 655        | 848              | 612          |
| SEQ SEQ X   | 98                 | 87         | 88         | 68                            | 06         | 16         | 92               | 93           |
| Vector  | Uni-ZAP XR         | Uni-ZAP XR | Uni-ZAP XR | 209148 Uni-ZAP XR<br>07/17/97 | Uni-ZAP XR | Uni-ZAP XR | Lambda ZAP<br>II | Uni-ZAP XR   |
| ATCC<br>Deposit<br>Nr and<br>Date   | 209148<br>07/17/97 | 209148     | 209148     | 209148                        | 209148     | 209148     | 209148           | 209148       |
| cDNA  | C1                 | HSAXI90    | HSAXN46    | HSDGW43                       | HSDJM31    | HSDJR23    | HSDMA90          | HSFAM73      |
| Gene  | 76                 | 77         | 28         | 79                            | 80         | 81         | 82               | 83           |

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Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic

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methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a

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combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

#### Signal Sequences

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Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, Virus Res. 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, Nucleic Acids Res. 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, supra.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., Protein Engineering 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty.

Accordingly, the present invention provides secreted polypeptides having a sequence

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shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., + or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

## Polynucleotide and Polypeptide Variants

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown inTable 1, the ORF (open reading frame), or any fragement specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the presence invention can be determined conventionally using known computer programs. A preferred method for determing the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result

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of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are:

Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignement of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence

except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted. (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%. 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be determined conventionally using known computer programs. A preferred method for determing the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuplc=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are

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considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the Nterminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or Ctermini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequnce are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as E. coli).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be

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deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions

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where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

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## Polynucleotide and Polypeptide Fragments

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity. More preferably, these polynucleotides can be used as probes or primers as discussed herein.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or

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the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.

Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

### **Epitopes & Antibodies**

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including

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monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')2 fragments) which are capable of specifically binding to protein. Fab and F(ab')2 fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and

#### Fusion Proteins

humanized antibodies.

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the

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polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

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Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

## Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1

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and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the

Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

### Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers,

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since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library).) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

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Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991) ) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In

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this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

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#### Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell. Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, 1311, 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of 99mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

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Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

### **Biological Activities**

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

### 35 Immune Activity

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the

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proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

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Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitis, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

## Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect

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interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstron's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

#### Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes

Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g.,

Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiollitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps,

Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention 15 include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, 20 Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Menigococcal), Pasteurellacea Infections (e.g., Actinobacillus, Heamophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases 25 or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, 30 Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria,

Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning.

Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria,
Leprosy. Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus,
impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases
(e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections.

A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

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Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or 10 diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

### Regeneration

A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteocarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue

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regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stoke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

#### 15 Chemotaxis

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotaxic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotaxic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotaxic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

#### Binding Activity

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

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(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

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Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

#### Other Activities

A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, caricadic rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

### 30 Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of

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positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type

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Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

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A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1: and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

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Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

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Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

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Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

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Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

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#### **Examples**

## Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

|    | Vector Used to Construct Library | Corresponding Deposited Plasmid |  |  |
|----|----------------------------------|---------------------------------|--|--|
|    | Lambda Zap                       | pBluescript (pBS)               |  |  |
|    | Uni-Zap XR                       | pBluescript (pBS)               |  |  |
| 15 | Zap Express                      | pBK                             |  |  |
|    | lafmid BA                        | plafmid BA                      |  |  |
|    | pSport1                          | pSport1                         |  |  |
|    | pCMVSport 2.0                    | pCMVSport 2.0                   |  |  |
|    | pCMVSport 3.0                    | pCMVSport 3.0                   |  |  |
| 20 | pCR <sup>®</sup> 2.1             | pCR®2.1                         |  |  |
|    |                                  |                                 |  |  |

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res.

- 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS.
- The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain

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DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR®2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported.

The oligonucleotide is labeled, for instance, with <sup>32</sup>P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

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Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 µl of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl<sub>2</sub>, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is

used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

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# Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

## Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P<sup>32</sup> using the rediprime<sup>TM</sup> DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100<sup>TM</sup> column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb<sup>TM</sup> hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

## Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions: 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on

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either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

## 5 Example 5: Bacterial Expression of a Polypeptide

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Ampr), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan<sup>r</sup>). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.<sup>600</sup>) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high

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affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acctate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM immidazole. Immidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

## Example 6: Purification of a Polypeptide from an Inclusion Body

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The following alternative method can be used to purify a polypeptide expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

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The cells are then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem

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columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A<sub>280</sub> monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5  $\mu$ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

# Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak Drosophila promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., Virology 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring

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signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μg of a plasmid containing the polynucleotide is co-transfected with 1.0 μg of a commercially available linearized baculovirus DNA ("BaculoGold<sup>TM</sup> baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One μg of BaculoGold<sup>TM</sup> virus DNA and 5 μg of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μl Lipofectin plus 90 μl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture

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and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200  $\mu$ l of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5  $\mu$ Ci of <sup>35</sup>S-methionine and 5  $\mu$ Ci <sup>35</sup>S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

## 20 Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSport 2.0, and pCMVSport 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

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Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No.209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (Sec. e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

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The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five µg of the expression plasmid pC6 is cotransfected with 0.5 µg of the plasmid pSVneo using lipofectin (Felgner et al., supra). The plasmid pSV2-neo contains a dominant selectable marker, the neo gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in 10 alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of metothrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 15 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1  $\mu M,$  2  $\mu M,$  5  $\mu M,$  10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 -200 µM. Expression of the desired gene product is analyzed, for instance, by SDS-20 PAGE and Western blot or by reversed phase HPLC analysis.

## **Example 9: Protein Fusions**

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

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Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

## Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACTCACACATGCCCACCGTGCC CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAAACC CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGT 20 GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAACCCCC ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT 25 GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA GGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC 30 ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

## Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera

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containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's

modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100  $\mu$ g/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

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Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

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It will be appreciated that Fab and F(ab')2 and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

# Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2 x 10<sup>5</sup> cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in

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Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-Iml PBS. Person A then aspirates off PBS rinse, and person B, using a12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl2 (anhyd); 0.00130 mg/L 15  $CuSO_4$ -5 $H_2O$ ; 0.050 mg/L of  $Fe(NO_3)_3$ -9 $H_2O$ ; 0.417 mg/L of  $FeSO_4$ -7 $H_2O$ ; 311.80 mg/L of Kcl; 28.64 mg/L of  $MgCl_2$ ; 48.84 mg/L of  $MgSO_4$ ; 6995.50 mg/L of NaCl;  $2400.0 \ mg/L \ of \ NaHCO_{3}; \ 62.50 \ mg/L \ of \ NaH_{2}PO_{4}-H_{2}0; \ 71.02 \ mg/L \ of \ Na_{2}HPO4;$ .4320 mg/L of ZnSO<sub>4</sub>-7H<sub>2</sub>O; .002 mg/L of Arachidonic Acid; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic 20 Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H<sub>2</sub>0; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-25 2HCL-H<sub>2</sub>0; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H<sub>2</sub>0; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalainine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 30 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tryrosine-2Na-2H<sub>2</sub>0; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 35 0.680 mg/L of Vitamin B<sub>12</sub>; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine;

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0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

## **Example 12: Construction of GAS Reporter Construct**

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

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The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proxial region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

|          | Ligand  | tyk2                         | JAKs<br>Jak l | Jak2             | Jak3                       | <u>STATS</u>                   | GAS(elements) or ISRE   |
|----------|---|------------------------------|---------------|------------------|----------------------------|--------------------------------|---|
| 5        | IFN family<br>IFN-a/B<br>IFN-g<br>II-10   | +                            | +<br>+<br>?   | -<br>+<br>?      | -<br>-                     | 1,2,3<br>1<br>1,3              | ISRE<br>GAS (IRF1>Lys6>IFP)   |
| 10       | gp130 family<br>IL-6 (Pleiotrohic)<br>Il-11(Pleiotrohic)<br>OnM(Pleiotrohic)<br>LIF(Pleiotrohic)                  | +<br>?<br>?                  | +<br>+<br>+   | +<br>?<br>+<br>+ | ? ? ? ?                    | 1,3<br>1,3<br>1,3<br>1,3       | GAS (IRF1>Lys6>IFP)   |
| 15       | CNTF(Pleiotrohic)<br>G-CSF(Pleiotrohic)<br>IL-12(Pleiotrohic)   | -/+<br>?<br>+                | +<br>+<br>-   | +<br>?<br>+      | ? ? +                      | 1,3<br>1,3<br>1,3              |   |
| 20       | g-C family IL-2 (lymphocytes) IL-4 (lymph/myeloid) IL-7 (lymphocytes) IL-9 (lymphocytes) IL-13 (lymphocyte) IL-15 | -<br>) -<br>-<br>-<br>-<br>? | + + + + + +   | ?                | +<br>+<br>+<br>+<br>?<br>+ | 1,3,5<br>6<br>5<br>5<br>6<br>5 | GAS<br>GAS (IRF1 = IFP >>Ly6)(IgH)<br>GAS<br>GAS<br>GAS<br>GAS<br>GAS |
| 25       | gp140 family<br>IL-3 (myeloid)<br>IL-5 (myeloid)<br>GM-CSF (myeloid)  | -                            | -<br>-<br>-   | ++++             | -<br>-<br>-                | 5<br>5<br>5                    | GAS (IRF1>IFP>>Ly6)<br>GAS<br>GAS                                     |
| 30       | Growth hormone fan<br>GH<br>PRL<br>EPO  | nily<br>?<br>?<br>?          | -<br>+/-<br>- | +<br>+<br>+      | -<br>-<br>-                | 5<br>1,3,5<br>5                | GAS(B-CAS>IRF1=IFP>>Ly6)  |
| 35<br>40 | Receptor Tyrosine K<br>EGF<br>PDGF<br>CSF-1   | inases<br>?<br>?<br>?        | +<br>+<br>+   | +<br>+<br>+      | -<br>-<br>-                | 1,3<br>1,3<br>1,3              | GAS (IRF1) GAS (not IRF1)   |

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To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is: 5':GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATGATTTCCCCGAAATATCTGCCAATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

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Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using Sall and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, Il-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

### Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml genticin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologics)

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with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required number of cells (10<sup>7</sup> per transfection), and resuspend in OPTI-MEM to a final concentration of 10<sup>7</sup> cells/ml. Then add 1ml of 1 x 10<sup>7</sup> cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

# Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

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The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells. Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2x10e<sup>7</sup> U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM Na<sub>2</sub>HPO<sub>4</sub>.7H<sub>2</sub>O, 1 mM MgCl<sub>2</sub>, and 675 uM CaCl<sub>2</sub>. Incubate at 37°C for 45 min.

Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

These cells are tested by harvesting  $1x10^8$  cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of  $5x10^5$  cells/ml. Plate 200 ul cells per well in the 96-well plate (or  $1x10^5$  cells/well).

Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

# Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon

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activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heatinactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a  $10\,\mathrm{cm}$  plate with cells around  $70\,\mathrm{to}~80\%$  confluent is screened by removing the old medium. Wash the cells once with PBS

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(Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as  $5x10^5$  cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to  $1x10^5$  cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

### Example 16: High-Throughput Screening Assay for T-cell Activity

NF- $\kappa$ B (Nuclear Factor  $\kappa$ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- $\kappa$ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- $\kappa$ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF-  $\kappa B$  is retained in the cytoplasm with I- $\kappa B$  (Inhibitor  $\kappa B$ ). However, upon stimulation, I-  $\kappa B$  is phosphorylated and degraded, causing NF-  $\kappa B$  to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF-  $\kappa B$  include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- $\kappa$ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- $\kappa$ B would be useful in treating diseases. For example, inhibitors of NF- $\kappa$ B could be used to treat those diseases related to the acute or chronic activation of NF- $\kappa$ B, such as rheumatoid arthritis.

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

### 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

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5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCC ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCA TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT AATTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTC CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAAGCTT: 3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF-κB/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF-κB/SV40/SEAP cassette is removed from the above NF-κB/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF-κB/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF-κB/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described

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in Example 13. As a positive control, exogenous TNF alpha (0.1,1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

#### Example 17: Assay for SEAP Activity

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15  $\mu$ l of 2.5x dilution buffer into Optiplates containing 35  $\mu$ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50  $\mu$ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50  $\mu$ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

| Reaction    | buffer Formulation.     |           |
|-------------|-------------------------|-----------|
| # of plates | Rxn buffer diluent (ml) | CSPD (ml) |
| 10          | 60                      | 3         |
| 11          | 65                      | 3.25      |
| 12          | 70                      | 3.5       |
| 13          | 75                      | 3.75      |
| 14          | 80                      | 4         |
| 15          | 85                      | 4.25      |
| 16          | 90                      | 4.5       |
| 17          | 95                      | 4.75      |
| 18          | 100                     | 5         |
| 19          | 105                     | 5.25      |
| 20          | 110                     | 5.5       |
| 21          | 115                     | 5.75      |
| 22          | 120                     | 6         |
| 23          | 125                     | 6.25      |
| 24          | 130                     | 6.5       |
| 25          | 135                     | 6.75      |
| 26          | 140                     | 7         |
| 27          | 145                     | 7.25      |
|             |                         |           |

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| 28 | 150 | 7.5   |
|----|-----|-------|
| 29 | 155 | 7.75  |
| 30 | 160 | 8     |
| 31 | 165 | 8.25  |
| 32 | 170 | 8.5   |
| 33 | 175 | 8.75  |
| 34 | 180 | 9     |
| 35 | 185 | 9.25  |
| 36 | 190 | 9.5   |
| 37 | 195 | 9.75  |
| 38 | 200 | 10    |
| 39 | 205 | 10.25 |
| 40 | 210 | 10.5  |
| 41 | 215 | 10.75 |
| 42 | 220 | 11    |
| 43 | 225 | 11.25 |
| 44 | 230 | 11.5  |
| 45 | 235 | 11.75 |
| 46 | 240 | 12    |
| 47 | 245 | 12.25 |
| 48 | 250 | 12.5  |
| 49 | 255 | 12.75 |
| 50 | 260 | 13    |

## Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO<sub>2</sub> incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is

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incubated at 37°C in a CO<sub>2</sub> incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10<sup>6</sup> cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10<sup>6</sup> cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca<sup>++</sup> concentration.

# **Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity**

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating

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tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford,MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford,MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 20 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na3VO4, 2 mM Na4P2O7 and a cocktail of protease inhibitors (# 1836170) obtained from Boeheringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract 25 filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g. 30

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and

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PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Bochringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg<sub>2+</sub> (5mM ATP/50mM MgCl<sub>2</sub>), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl<sub>2</sub>, 5 mM MnCl<sub>2</sub>, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30°C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mm EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavadin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phospotyrosine antibody conjugated to horse radish peroxidasc(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

## 25 Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

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Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at  $4^{\circ}$ C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

### Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR

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products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Manheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

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## Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

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The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

#### Example 23: Formulating a Polypeptide

The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1  $\mu$ g/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1  $\mu$ g/kg/hour to about 50  $\mu$ g/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracistemally, intravaginally,

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intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), bucally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or mirocapsules. Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481). 10 copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988). Sustained-release compositions also include liposomally entrapped 15 polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes 20 are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

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#### Example 24: Method of Treating Decreased Levels of the Polypeptide

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It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

#### Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

#### Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days.

After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

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pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other

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disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties.

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### INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

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| Address of depositary institution (including postal code and coll 10801 University Boulevard Manassas. Virginia 20110-2209 United States of America  | ountry)   |
| Date of deposit July 17, 1997  | Accession Number 209147   |
| C. ADDITIONAL INDICATIONS (leave blank if not appointed appointed and appointed appointed and appointed ap | TIONS ARE MADE (if the indications are not for all designated States)   |
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(PCT Rule 13bis)

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#### What Is Claimed Is:

- 1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:
- (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;
  - (f) a polynucleotide which is a variant of SEQ ID NO:X;
  - (g) a polynucleotide which is an allelic variant of SEQ ID NO:X;
  - (h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
- (i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.
- 2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.
- 3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

- 4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.
- 5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
- 6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
- 7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.
- 8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.
  - 9. A recombinant host cell produced by the method of claim 8.
  - 10. The recombinant host cell of claim 9 comprising vector sequences.
- 11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:
- (a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;
- (c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.
- 12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.
- 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.
- 14. A recombinant host cell that expresses the isolated polypeptide of claim 11.
  - 15. A method of making an isolated polypeptide comprising:
- (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
  - (b) recovering said polypeptide.
  - 16. The polypeptide produced by claim 15.
- 17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.
- 18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
- (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.
- 19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
- (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

- 20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:
  - (a) contacting the polypeptide of claim 11 with a binding partner; and
- (b) determining whether the binding partner effects an activity of the polypeptide.
  - 21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.
- 22. A method of identifying an activity in a biological assay, wherein the method comprises:
  - (a) expressing SEQ ID NO:X in a cell;
  - (b) isolating the supernatant;
  - (c) detecting an activity in a biological assay; and
  - (d) identifying the protein in the supernatant having the activity.
  - 23. The product produced by the method of claim 22.

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| cacgegteey | ggaagatgag               | gaggtcqctg               | agagetggga                              | agaggeggea              | cetteccucu               | 100  |
| aggaaatcca | aatctcctcc               | caaagtgccc               | artglgatic                              | aggacyatag              | cctccccgcg               | 240  |
| ggyccccctc | cacagateeg               | catectcaag               | aggcccacca                              | gedaeggege              | agagggggg                | 300  |
| cccaactcca | ccagcaggcc               | caccetteca               | gtcaagtccc                              | Lagcacageg              | agaggeegag               | 360  |
| tangccgagg | cccggaagcg               | gatcctgggc               | agcgccagcc                              | ccgaggagga              | acceatast                | 400  |
| occatected | acaggccaac               | caggatetee               | caacccgaag                              | acagcaggca              | geceaacaac               | 480  |
| gtgatcagac | agcctttggg               | tcctgatggg               | teteaagget                              | tcaaacaycy              | cagacaaacg               | 540  |
| caggcaagaa | aagatgccgc               | cgttgctgcc               | gtcaccgcct                              | cotgggtcgt              | ttacttccac               | 600  |
| ttgcantgcc | gtggcagaca               | gctggacttg               | agcagaggga                              | acgacctgac              | acctegede                | 650  |
| tgtgatecec | cttgctccgc               | ccactgtgac               | cetgaacccc                              | tataacaaat              | gaatggaaag               | 720  |
| ttatacccat | tcccactgtg               | attggcacat               | cgacaagggc                              | aggactcage              | agagtcagac               | 780  |
| ggaaagggtg | ggggttaggg               | gaaggttggg               | gggacceage                              | tangagttta              | teatecteat               | 840  |
| agtgccactt | ggccacttgg               | ggtaaagcca               | gegecageaa                              | caacagccca              | agtgcatgtc               | 900  |
| taatttggga | tttcaaaaca               | caaatgaaaa               | ctcacaccca                              | tottttt                 | tretteetat               | 960  |
| tccatcactt | aaaaagtaag               | ttccatttga               | aaatateett                              | tagatagaa               | gagtttagt                | 1020 |
| ttttgtttgt | ttatacaaat               | atctgatttg               | caayaaaaay                              | totacttaaa              | aatgtttctg               | 1080 |
| ggtttaatga | atttttaatt               | aagaaagggt               | agiliggiag                              | gettagette              | totattocta               | 1140 |
| ggaaattcac | tagaaacatt               | aaccaatagg               | accordage                               | acadacdadc              | accccatgcc               | 1200 |
| ctgccgccca | gaaaaggggc               | agggctctgc<br>aagtcccagg | agecyceagg                              | cttacctaga              | gactgggcta               | 1260 |
| tatacctccc | teecegaget               | gggagggtgc               | caaccccacc                              | totagtattt              | tgggagatag               | 1320 |
| getetgtagg | cccggagecg               | cttcccatac               | ccctcagggt                              | ggttccctac              | cagccaggct               | 1380 |
| ggaaagtgaa | ccgacttecc               | agagtgccag               | ggagtgagat                              | tocatcccto              | ggcttagaag               | 1440 |
| tactactict | ayaayaaayc               | tagtattttg               | ccatcagcac                              | aaggaaaacc              | aggagagagt               | 1500 |
| chacqqaqaq | aagacttgtt               | cttctgcctc               | gratgttcag                              | aaggtggata              | ggtcttccca               | 1560 |
| ctgccccag  | gactetgage               | ttaggggtct               | gcagtgctcc                              | atctccattg              | gtggccccag               | 1620 |
| ctcageatg  | atacctedta               | catttcctgt               | gtgcaatcag                              | taccttgaag              | gcagaacatt               | 1680 |
| ctcagtaacc | ttqqaaaaar               | aamaaaaaaa               | aaaaaaaaaa                              | aaaaaaaaa               | aaaaaaaaa                | 1740 |
|            | aaaaaactcg               |                          |   |                         |                          | 1761 |
|            | _                        |                          |   |                         |                          |      |
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| <110> 12   |                          |                          |   |                         |                          |      |
| <211> 1519 | )                        |                          |   |                         |                          |      |
| <212> DNA  |                          |                          |   |                         |                          | -    |
| <213> Homo | sapiens                  |                          |   |                         |                          |      |
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| <400> 12   |                          |                          | 000000000000000000000000000000000000000 | · actaactcca            | actcacqaaa               | 60   |
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| cageceeggg | g egeogegeeg             | , cectyageee             | : ageeteetas                            | ccattttcta              | aaaaagcagg               | 180  |
| £gagggraja | aggorages                | g caggeeegge             | . daegeedda.                            | . aaaaaaaaaa            | aagetgetge               | 2.40 |
| gagcagagct | . ccccccccg              | . cyccyacyca             | tetestttt                               | ccadactact              | teceteeg                 | 300  |
| cttttgcgct | ggagattey                | gggcaaggct<br>taaggaaaa  | acctagaaa                               | tagagcagac              | : ctggacgaga             | 360  |
| ggtgaggag  | geddigagad<br>Gaeagagata | taayyaaayo               | r gtaccada                              | cgguscasa<br>cgagtcacac | agcagctttt               | 420  |
| gattatttt  | g cayayyatga             | a addocetec              | , glacceagae<br>a atacaatca             | agatotgga               | agcagctttt<br>aagtggtgaa | 430  |
| cttagtgaca | a ctaaayatco             | ayyuuuuu<br>aatattootto  | . gogodgood<br>. adagcattt              | r agaaaccccc            | tcaggtacag               | 540  |
| aaggtcccg  | c ttgtgtagat             | t transarra              | , dydyddiae;<br>chaatdac                | tgaagaagg               | a gaacttcagc             | 500  |
| acccagget  | a kastatsati             | t cataaaaaa              | r cacatacaa                             | agaagtatg               | a ggccagccgg             | 560  |
| cicaagetg  | t acasacaca              | a cactgaggag             | , egeatgeaa.<br>Taaggttgaac             | g tggagagett            | gaaacgagaa               | 720  |
| gaggacatc  | a adaaacado              | a totodataa              | a acatooocto                            | g atgtggagaa            | a totcaacagt             | 780  |
| caccaygac  | a ctalactic              | a acaccaatti             | caggagcga                               | cacagkgagad             | ggagcatgtt               | 340  |
| cagaacgaa  | 5 CC349CCCC              | J J J J                  | 2 22 2 2                                |                         |                          |      |

```
900
tatgagetet tggagaataa gatscagett etgeaggagg aatecagget agcaaagaat
                                                                    960
gaagetgege ggatggeage telggtggaa geagagaagg agtgtaaeet ggagetetea
gagaaactga agggagtcac caaaaactgg gaagatgtac caggagacca ggtcaagccc
                                                                   1020
gaccaataca ctgaggccct ggcccagagg gacaagtagg tgccttcggt gctctttttg
                                                                   1030
togottgtot titgoccatt otcaaggoat acagoagotg tootgttoco titcaaggao
                                                                   1140
tgacagtagg agetteaeta titetaagae titatggger cacaacegaa qacattetti
                                                                   1200
tcagggttga attttcagtg gtatccatta tgaaaactca cttcatggat tcagtgggca
                                                                   1260
aatageggea ageaagagae atqgatteae ttatteggea aacatttaet gggeatgeea
                                                                   1320
catgecagat accgggetaa gtatetggea tgtgttaeag aaacaaaaga eetaaatett
                                                                   1380
gtcaccaaga aacatgttac atgattttaa raagttccct gataqaaqaq catggggtgc
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                                                                    120
                                                                    180
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gggtggattc taagaccctg acccgtaaca cgaggatcat tgcagaggcc ctgactcgag
                                                                    240
                                                                    300
 tcatctacaa cctgacagag aaggggacac ccccagacat gccggtgttc acagagcaga
                                                                     360
 tgatccagca ggagcagctg gactcggtga tggactggct caccaaccag ccgcgggccg
                                                                     420
 gcagetggtg gacaaggaca gcacetteet cageaegetg gageaecame tgagemgeta
                                                                     480
 cctgaaggac gtgaagcagc accacgtcaa ggctgacaag cgggacccag agtttgtctt
                                                                     540
 ctacgaccag ctgaagcaag tgatgaatge gtacagagte aagccageeg tetttgacet
                                                                     600
 geteetggee gttggeattg etgeetaeet eggeatggee taegtggetg teeageaett
                                                                     650
 cagectecte tacaagaceg tecagagget getegtgaag gecaagacae agtgacaeag
                                                                     720
 ccaccccac agccggagcc cccgccgctc cacagtccct ggggccgagc acgagtgagt
                                                                     780
 ggacactgcc ccgccgcggg cggccctgca gggacagggg ccctctccct ccccggcggt
                                                                     840
 ggttggaaca ctgaattaca gagctttttt ctgttgctct ccgagactgg ggggggattg
                                                                     900
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 caggetacgg acttgcggac gagecececa gteetgggag ceggeegeec teggtetggt
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                                                                    1020
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 ctagagaccg gggccggaga cgtggcagcc gccctgcccg ccagaaagtt tcctagaagt
                                                                     180
 ttgctgggcg cgggcgcacg actgactggc tggaccatga acgtgttccg aatcctcggc
                                                                     240
 gacctgagec acctectgge catgatettg etgetgggga agatetggag gtecaagtge
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300
tgcaagggca tototgggaa gagocagato otgtttgoto togtottoac caccaggtac
ctggacctgt tcaccaactt catctccatc tacaacacag taatgaaggt ggtttttctc
                                                                      360
                                                                      420
ctotgtgoot atgttacagt gtacatqata tatgggaaat toogtaaaac ttttgacagt
gagaatgaca cattoogoot ggagtttott otggtoocag toattggoot ttoottoott
                                                                      480
gaaaactaca gtttcactct gctggagatc ctctggactt tctctatcta tctggaatca
                                                                      540
                                                                      500
gtggctated tgccccaget chicatgate ageaagactg gagaggetga gaccataact
acteactace tgttetttet gggtetgtae egggeactet acetggetaa etggateagg
                                                                      663
cggtaccaga ctgagaattt ctatgaccaa attgcagtcg tgtctggagt agtacaaacc
                                                                      720
atottotact gtgacttott ctacttgtat gggaccaaag gtaggtootg ggatgacago
                                                                      780
aatgetgaca etggeetaag gagttaetea teeatttaat aagtatteea geagataeag
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                                                                      180
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                                                                      240
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ccccatcccc agctgggaag aacatgctat ccaatctcat ctcttgtaaa tacatgtccc
                                                                      300
                                                                      360
cctgtgagtt ctgggctgat ttgggtctct catacctctg ggaaacagac ctttttctct
                                                                      420
cttactgctt catgtaattt tgtatcacct cttcacaatt tagttcgtac ctggcttgaa
getgeteact geteacacge tgeetectea geageeteac tgeatettte tetteecatg
                                                                      480
caacaccctc ttctagttac cacggcaacc cctgcagctc ctctgccttt gtgctctgtt
                                                                      540
cetgtecage aggggtetee caacaagtge tetttecace ecaaagggee teteettte
                                                                      600
                                                                      660
tocactgica taatcictit coatcitact tgcccticta tactiticica catgiggete
cccctgaatt ttgcttcctt tgggagctca ttcttttcgc caaggctcac atgctccttg
                                                                      720
cetetgetet gtgcacteae geteageaca catgeateet ecceteteet gegtgtgeee
                                                                      780
                                                                      840
actgaacatg ctcatgtgta cacacgcttt tecegtatge tttetteatg ttcagtcaca
                                                                      900
tgtgctctcg ggtgccctgc attcacagct acgtgtgccc ctctcatggt catgggtctg
cccttgagcg tgtttgggta ggcatgtgca atttgtctag catgctgagt catgtctttc
                                                                      960
ctatttgcac acgtccatgt ttatccatgt actttccctg tgtaccctcc atgtaccttg
                                                                     1020
                                                                     1080-
tgtactttct tcccttaaat catggtattc ttctgacaga gccatatgta ccctaccctg
                                                                     1140
cacattgtta tgcacttttc cccaattcat gtttggtggg gccatccaca ccctctcctt
gtcacagaat ctccatttct gctcagattc cccccatctc cattgcattc atgtactacc
                                                                     1200
                                                                     1260
ctcagtctac actcacaatc atcttctccc aagactgctc ccttttgttt tgtgtttttt
                                                                     1320
 tgaggggaat taaggaaaaa taagtggggg caggtttgga gagctgcttc cagtggatag
 ttgatgagaa tootgaccaa aggaaggcao oottgactgt tgggatagac agatggacct
                                                                     1380
 atggggtggg aggtggtgtc cetttcacac tgtggtgtct cttggggaag gatctccccg
                                                                     1440
                                                                      1500
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 aaactcga
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<210> 16

<211> 2006

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

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\langle 222 \rangle (70)
\langle 223 \rangle n equals a,t,g, or c
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<212> DNA
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<223> n equals a,t,g, or c

<220>
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<221> (530)
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<223> n equals a,t,g, or c

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                                                                  120
aggagcagat cagcaatgag ggtgaggaca aaatcttctt aatcaacaag ettcaetcca
                                                                  180
                                                                  240
tetacgagag gaaggagagg gaggagagga geagqqttgg gacaaccgag gaggetgegg
vaccocotgo cotgotoaca gatgaanayg atgootaygg ggaeggegat gggcotnang
                                                                  3:0:0
ggccsgccca gcaccctgag accacactgt tgcctcccag tgaccctgct gggacaccag
                                                                  350
gacaaggaag acagtttege etetegaaag eegeagetge geetaggetg gagetggaag
                                                                  420
ggtgggtgaa tooggottgg goatococaa tgaactotgo cotgootggg actotattla
                                                                  480
tictgattaa aqqqgttttg caaatgaaaa aaaaaaaaa aaaaaaaccn cggggggggn
                                                                  540
                                                                  545
ccggn
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                                                                   120
ggaagetetg taaccaccag caagaccaga agtggggtga teageagtge aggaaageee
                                                                   180
 atttgggtgc aqtccccgca cctagccctt ttggaagtgc ttctccaaaa gggaattgtg
                                                                   240
 ceggaaaagt agggattgaa accaaacage cacateetge cateaggatg etetttatgg
                                                                   300
 ceceaetgae caagaaatea cagettetgt aeteagtgat gaetgettga etteagttga
                                                                   360
 ggaaaacaat gaagttetgt agecaggegt ggtggeagat gtetgtaate eeagetaete
                                                                   420
 gggaggctga ggcaagagaa ttgcttaaac cccgggaggt ggaggttgca gtgagccgag
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 600
                                                                   602
 σa
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 <211> 587
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 <213> Homo sapiens
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                                                                   120
 aagaatttgt gcacaaaagt cttaactgtt ttgcagcctt ggttgtggtt agatgctgta
                                                                   1.80
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                                                                   240
  ttagtttaac tgttagttta aagtcagttt ctatagcgge acagtcttta tttttggacc
                                                                   300
  tteactttcc aatccagatg acacttgtcc ataaagaaat tgctaaactt gagacctaaa
                                                                   360
  aacaaaacaa aaaacaaaaa aactacagac aagtaacctt taaaattatt tcgcttgatg
                                                                   420
  gaaatttacc ggaaggcttt aaccaattca gtttgcttag actcataaag aaaattatga
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<211> 644
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tettacagtg caagagtett tacaagacee tacaatacat gatetteete geageatttt
                                                                                                                                    120
additionable tattion and additionable transfer additionable additionab
                                                                                                                                    180
tigitgitto tigitaracti atcagacaca ticitocoto aagotatiig tattigotat
                                                                                                                                    240
tecttcaaat aacettatag ettgiletta acateettea aaceattget cagatgiaca
                                                                                                                                    300
ettecacatg actetttace ttaacactaa caaaaataaa eegtetgeee tglactetet
                                                                                                                                    350
etttttetge tttattteea ecceatatae ttatggeett caaatatget ataaatgttt
                                                                                                                                    420
                                                                                                                                    480
ttttatttat atttttgtta tetgteteta etaaaaatae aaaaattage tgggtgtget
ggctggcacc tgtaatccca gctacttggg aggcttaggc agaagaatca cttgaacctg
                                                                                                                                    540
ggaggeagag gttgeagtga getgagateg egecaetgta etceageetg ggeaacagga
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<213> Homo sapiens
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                                                                                                                                     120
 aaaaggagag gtagatacag tcagtgtcac ttcaggacac ttaggttttt tttgtataaa
                                                                                                                                     180
 aatttaaatt gaattaaaag aaggaaaaaa aaagcccaaa cttaacctct gagaaagaac
                                                                                                                                     240
                                                                                                                                     300
 ataagaactc aaggagaaca taagagaaaa ggaaacctgt tacagaaaag acaagaatct
 gtgttttgga atgagtctat tcttgggtat tgaactttta gttttgtttg cccaaggatt
                                                                                                                                     360
 aattgaggaa atcagctaag aaaatggact ttagacaaaa gcaagaggat cagatgaaga
                                                                                                                                     420
 aaaggagagg tagatacagt cagtgtcact tcaggaaagc tatttaaaaa aacttgaaat
                                                                                                                                     480
                                                                                                                                     540
 ttaactgaaa gaagaaacaa caacaaaaaa gcctaaacct agcctctgaa caacactaac
 atgagaacac aagaacttaa gagaaaaaga aacctactca agaaaagaca gaagagacag
                                                                                                                                     600
 tgatttggga tgagtctact ctaggatttt caacttttta gttttgttcc ttcaaagttg
                                                                                                                                      660
                                                                                                                                      720
 aaggaaaaaa agtttggttt tataaaattc atgttattgt aatttttcta ggtggatggc
                                                                                                                                      780
 tattttaatc tctaaaaaag ccaagtgaag taaaagtatt cagtatgcct tttcctcaag
  ttactttcct tcattttctt aaaaaaraaa aaaaattatt aaatgtttct cacatatctc
                                                                                                                                      840
                                                                                                                                      900
  acatataatg taattteeet aaatgaagtt gtetetaett etgeteatea aattgetgtg
                                                                                                                                      960
  atagtgaatt atttattcat gggagataat ttattttaaa ggacagaatt accaagcgtt
                                                                                                                                    1020
  acaaaatcag ttotttoott ggttttgtgt tagtgttggt ggtattttat tgttgttttt
  ctgtgtttat gtgtctcagc tttctccaag gaatatgtat gaaataactt aaactgattt
                                                                                                                                    1080
  tttctttgtt aaatctaatt tgcagtgtat ttttgcattt tctagttctg aaagtggaaa
                                                                                                                                    1140
  atgaaacagt ctataataaa cttagatgat atatagtttt aaaacggtct caaaaagtac
                                                                                                                                    1200
  tgatataagg tcagtctata ttctggaaat gtttatatta aagtgtttta atttcta
                                                                                                                                    1257
  <210> 22
  <211> 541
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<220>

<221> SITE

<212> DNA

<213> Homo sapiens

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ctaragouaa gttagatttq ggggttattc agccaaaatt accgttttag accaqaatga
                                                                       120
atagactaca etgataaaat gtaetggata atgecaeate etatatggtg ttatagaaat
                                                                       180
agtgcaagga aagtacattt gtttgcctgt cttttcattt tgtacattct tcccattctg
                                                                       240
tattottgta caaaagatot cattgaaaat ttaaaagtoat cataatttgt tgocataaat
                                                                       300
alglaagtgt caataccaaa atgtotgagt aactfoltaa atcoctqtto tagcaaacta
                                                                       350
atattggtto atgtgcttgt gtatatgtaa atcttaaatt atgtgaacta ttaaatagac
                                                                       420
cctactgtac tgtgctttgg acatttgaat taatgtaaat atatgtaatc tgtgacttga
                                                                        480
tattttgttt tatttggcta tttaaaaaca taaatctaaa aaaaaaaaa aaaaaactcg
                                                                        540
                                                                        541
<216> 23
<211> 567
<212> DNA
<213> Homo sapiens
<400> 23
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                                                                         60
aacatgctcc gtataaaaag ttgtctctta ttatttttta tttttttcc atttaacatt
                                                                        120
aaagactctc aagtacctgc caattatatt gccacatttt ctaggaaatg cagcttttag
                                                                        180
caattetttg ttgatteaaa tgaaateaae etageteage taatattaat tgattagatt
                                                                        240
gagaataaag teetaataee aaaggetgae caagagaaaa tgettgaaat cagatgttga
                                                                        300
ctgattcagg ccggttctat cagtttgggc aagttgctag ggagtggaca ggaagcttga
                                                                        360
 ggacatcaca aaagaatcca taaaggaccc atgatgcatt gagagacaga tacataagaa
                                                                        420
 tggctgggca tagtagaaca gatctggtat cattacagta aatctccatt atatggagtt
                                                                        480
 atctagaaac attatcttcc ttgctggctg aagaaacata gtacccctcc aactaccctc
                                                                        540
                                                                        567
 aaacaaaaaa aaaaaaaaa actcgta
 <210> 24
 <211> 586
 <212> DNA
 <213> Homo sapiens
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 <221> SITE
 <222> (1)
 <223> n equals a,t,g, or c
 <220>
 <121> SITE
 <222> (28)
 <223> n equals a,t,g, or c
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 <221> SITE
  <222> (550)
  <223> n equals a,t,g, or c
  <400> 24
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neegetetta gaactagtga tecceegnge tgeaggetgg ggggeteegg tteeetgagg
                                                                        60
gatgageett cageeteeet tigtaatget geteetetee aetgeeeage aecatgagit
                                                                       120
gggtgeagae acctagaagg agagaettet tggaaegete atceeeeget ataeetenee
                                                                       180
ttectectgr atotecectl officettee ecoleaggag agagaaaatt tagtgettre
                                                                       240
agosottett ggageettea tggtecaggg gtaggggeee caetggeetg ageatgeeat
                                                                       300
tttgagggga gggtagttqt geetaettat edeetggeag aggggatgee aggaeeatgg
                                                                       360
                                                                       420
acatgagget tgeccatece tgecaactta cacageetgt accaetgtee eccetteett
                                                                       480
ggctactttg acatgtgcct gctcctggca tttcaataaa acccggcttg ggtctgaaaa
                                                                        540
aaaaaaaaaa aaaaaaacto gaggggggc cggtamccaa ttogcoctat artgaatogt
                                                                        586
attaaaattn aatgggoyyt ogttttacaa agtogtgact ggggaa
<210> 25
<211> 1510
4.112> DNA
::13> Homo sapiens
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                                                                         50
 cgggcagaac aagcggccgc caagctgggc magatcggcc ggagcaagcg ggttgttatt
                                                                         120
 gaagatgata ggattgatga egtgetgaaa aatatgaeeg acaaggeaee teetggtgte
                                                                         180
 taactccccc aaagacaatg agttaaggga gagaataaga acggcggtaa cagttattgg
                                                                         240
 caaaaagcat gaaaagagaa agcactttga aatttattac tagcttgcta cccacgatga
                                                                         300
 aatcaacaac ctgtatctgg tatcaggccg ggagacagat gaggcgagag gaggaggagg
                                                                         350
 aggaggagaa ggctctgggc tcctctgcaa aaataaaaat aaaaaaataa ataaaatttt
                                                                         420
 aaaaataata aaaattcact atatacacat ataaagaaat aaaaagaagt ctcagttgca
                                                                         430
 gctatttgtc aaaattaata tccatttctt tttatatacg gtgaatattg cgcaattata
                                                                         540
  gatetggatt ttgaaccact taatgaageg geaacaceag gtgttttgag gtgttggeat
                                                                         600
  tettegetga titiggetgit eccaatgitt acattatita atetigeaaa aatggitetg
                                                                         660
  tgcacttgga tgtgaaatgc tgtccagttt tattttttt atgttgttat ccttggatgt
                                                                         720
  acaaaaaatt cagaaaatga tctctgtaga tattctgttt tattttggtc atctttagaa
                                                                         780
  gttatcagga atgtgtttaa aacaagaaga gaacttttct aaggaatgat acatagaaaa
                                                                         840
  gattttattt taaaatgagt tgtaaagctt gtgtttcttt gttgctgcaa gctatctgcc
                                                                         900
  caagttaatg caaatggaca catttttat gtcagaaaaa cacacacaca cacacacaca
                                                                         960
  cacacacaca cacacacaca cgaaaaacaa agaaaaaaat gcttgagctt tttctaactt
                                                                         1020
  cecettgcag tetgttgtgt gageageetg tttatttete taatattatg teagtttatt
                                                                         1080
                                                                         1140
  ctctttaatg gactgtaaaa aaatgtaatc acaagagtgc caaatatctt gaaatgccaa
  aaggcatttt agtttetttt etetgtgete tgagteeacg taeaggaatg ettggagtgt
                                                                         1200
  cttttctgtt atttataggg attctcttaa ggcacaccag ctgcctgttt tgcatggtat
                                                                         1260
  ttgcaaaaat geetettgeg tgaggaaate ttttaccatt ttttgtttge aactttggae
                                                                         1320
  ctcaagaggt ttcccttccc ttccccgttc cctcttttct taattcaata ttctgtatgt
                                                                         1380
  tgcaccttga accagcacac agggetattt etecaatgta caataaaaga attgtteetg
                                                                         1440
  tgtctcaaaa aaaaaaaaaa aaaaaaactc gagggggggc ccgtacccaa tcgcctratg
                                                                         1500
                                                                         1510
   atcgtatagc
```

<210> 26 <211> 535

<212> DNA

<213> Homo sapiens

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<2001 - SITE
< 2112 + (523)
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                                                                         60
grgccccggt caggecctge ccagagaget netggtteet gaactgaget geetetaccg
                                                                        120
tggtgggctg ggcaggcatg tgccccccta gtcagagggc accaacccac ctactctgcc
                                                                        180
cotgggtgga tootgggccg glogtgttag ggttgtccct ctgggtgctg qctggtggga
                                                                        240
tgggkgaggg tggggagcag ctcccagcac ccctgctgtg tggttcatct tttttttagg
                                                                        300
decetgeetg tetgeecate tgeeceteae ceaecetagg etetgeecae egeetggace
                                                                        360
tgcccacccc tgaaagactg gcccctggct ccccgcccct cggtctccac gtggtgtatg
                                                                        420
gatetgtggt cattgteect etgeagaata aagattgete aggeetgeet ggaaaaaaaa
                                                                        480
adadadada adadadadat cqaqqqqqqqq cccqtaccca atcqcctqnq atgat
                                                                        535
<210> 27
 <211> 1273
 <212> DNA
 <213> Homo sapiens
 <400> 27
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                                                                          €.0
 teggeggetg atttagaagg aggtteagge taeggtgage egaagggagg attetggett
                                                                         120
 occetytecy tyttecatet agecaeaag gagecatyga agtygeagag eecageagee
                                                                         180
 ccactgaaga ggaggaggag gaagaggagc acteggcaga gccteggccc egcacteget
                                                                         240
 ccaatcctga aggggctgag gaccgggcag taggggcaca ggccagcgtg ggcagccgca
                                                                         300
 gcgagggtga gggtgaggcc gccagtgctg atgatgggag cctcaacact tcaggagccg
                                                                         360
 geoctaagte etggeaggtg eccegecag eccetgaggt ecaaattegg acaecaaggg
                                                                         420
 tcaactgtcc agagaaagtg attatctgcc tggacctgtc agaggaaatg tcactgccaa
                                                                         480
 agetggagte gttcaacgge tecaaaacca acgeeetcaa tgteteecag aagatgattg
                                                                         540
 agatgttcgt gcggacaaaa cacaagatcg acaaaagcca cgagtttgca ctggtggtgg
                                                                         600
 tgaacgatga cacggcctgg ctgtctggcc tgacctccga cccccgcgag ctctgtagct
                                                                         660
 geetetatga tetggagaeg geeteetgtt eeaeetteaa tetggaagga etttteagee
                                                                         720
 tcatccagca gaaaactgag cttccggtca cagagaacgt gcagacgatt cccccgccat
                                                                         780
                                                                         840
  atgtggteeg caccateett gtetacagee gtecacettg ceageeceag tteteettga
                                                                         900
  eggageceat gaagaaaatg tteeagtgee catatttett etttgaegtt gtttacatee
  acaatggcac tgaggagaag gaggaggagg atgaagccat tgaggttgag gccactgtct
                                                                          960
                                                                         1020
  gaaccatccc tgtacatctg caccttcttg tgcaaggaag tccttggcct aaagccttgg
                                                                         1080
  ttotcaaact gggttoottg ggacotoogg ggtggggggg ttocaggagg caogtagggt
  accttgcagg gtcctaggag ggaaacccag gattccagga gggatcccag gaactgtggg
                                                                         1140
  cacccatttt ctgtgtctcc cagcccattt ccactcctag tttgtcatgg ataatttttg
                                                                         1200
                                                                         1260
  ttetteeetg tgtgattttt gecateaaaa taaaaaatltg agaetegtta aaaaaaaaaaa
                                                                         1273
  aaaaaaaact cga
  <210> 28
  <211> 780
  <212> DNA
  <213> Homo sapiens
   <400> 28
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                                                                            60
```

| cccggacct gtggatgeeg atecaggtta tggggggege rteagecagg cegteegete gtgteaggtg tegetagtg eteagagget geeacetgee agectgggaa ggeeggtga actgeacetg geagaggagt gaagatgtg eteaaaqtee egttagggtg eeageteet tgegaggget etgagggetg tggggeeea gtetteaaca catettagt eteteteaq taagectgea tgggagteen ggaaggtee   | a ggatgactca ggegagecag aggaetgggt a gettgeeca catggteect tteaceagtg c tggaeteate cettgteaca gagettgget t tgagggtgte aaaggteagg geagtgetee t gggetgttt cetetgtgge tggteactet c ttetgagetg tggggtgtee etgeecegee g gtgaeceetg agetetgtae tgatttggge g etcagagece atetgtgeet ggeectegte g geetggeece tgeectggea cagatggtaa a ggaaaacee aggaeetttg gettgteece c tgtggggta gagggetgg ggattgaage c egggaggete aggeetgete ecageetega  | 120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780              |
|---|---|---|
| <210> 29<br><211> 819<br><212> DNA<br><213> Homo sapiens  |   |   |
| gcaactgctg cetttgttge ttatactge gctaagaaac atteaggeeg gcageagea gggeetgaga aageagteet atetteagt acaacgtatt caaggtetga gtgccacgt gceettteag etectaceag cagactate gctetggggg eggegteage acactgate ggcactagea aagaagettg gaaatagaa acaccaeggt etgeeetgea aaaacacca cacteetcaa aaaaagaact ttggetgal agacttgaca attetgttet ggteaagee cagaagacat cageeaactg caegagtee | te tggctggca tgctggcctg tgtcttectg tg cagagagcag agagcactge aaccagacct tg gctacaggca gttcccctg cattacettg tg gacttcttca ggactccaga ggaggcccac ta gtgaaacagc tggtcatccg cegtgggct tggggctcac ggtcaggate ctagccacca ta gccaggagtg gctgtccca gtatgcaacca ta gcgggtctag tgcaggtga cactttgaac ta tggggtctag tgcaggtga cactttgaac ty cettgtggtg acactcagag gggtctgaac tg gagttttctt ctgtgacttg gactgctcta ag agtccaggga ttgtcactat tattaataat at aammycacaa aaaccactgt tatattaaag aa aaactcga | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>819 |
| <210> 30<br><211> 608<br><212> DNA<br><213> Homo sapiens  |   | -   |
| ccccaggaga ctctaccca actcagcc<br>cagtgcctga agaatatqat ccaaactt<br>gtgctggacc tggcccttgc ttctgctc<br>gttttcttcc ttccccacaa ggccagca<br>accagtgagc wcaccaggaa cttctgct<br>qtctcccat gctgcttcta acccaaat<br>agagccaggc acagcagtac acgcctct  | ce eteteetgea cacacacaa cacacacaa aacaccaqueg aacaacette agtggeteec ete ectgeetace tetgtettee cetttttac etetgtettee ectetgacat aatateacet ectecaggaa gteeteeatg et tgageecea gaaagagea tgetgeagaa agtacaggag aggagtteag gaaaaagtet ectecagetam tegggagget gaggtgggag aacactgttte ttaaaaaaaa aaaaaaaaaa aaaaaaaaaa   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>608                      |

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<210> 31
<2111> 1217
<212> DNA
<213> Homo sapiens
<400> 31
                                                                        60
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                                                                        120
gecaccaget tggaetteta gggaetttee teteagecag gaaggatttt gatatteate
                                                                        180
agaaatacct ccagaagatt caaggagntg tagaggtgaa qtaagcctgt gaaggaccag
                                                                        240
catgggaate ctatactetg ageceatetg ccaageagee tatgeagaat gaetttggae
                                                                        300
aagtgtgggg gtgggtgaaa gaagacagca gctatgccaa cgttcaagat ggctttaatg
                                                                        360
gagacacgcc cctgatctgt gcttgcaggc gagggcatgt gagaatcgtt tccttccttt
                                                                        420
taagaagaaa tqctaatgtc aacctcaaaa accagaaaqa gagaacctgc ttgcattatg
                                                                        480
ctgtgaagaa aaaatttacc ttcattgatt atctactaat tatcctctta atgcctgtyc
                                                                        540
tgettattgg gtattteete atggtateaa agacaaagea gaatgagget ettgtaegaa
                                                                        600
tgctactiga tgctggtgtc gaagttaatg ctacagattg ttatggctgt accgcattac
                                                                        660
attatgcctg tgaaatgaaa aaccagtctc ttatccctct gctcttggaa gcccgtgcag
                                                                        720
accccacaat aaagaataag catggtgaga gctcactgga tattgcacgg agattaaaat
                                                                        780
tttcccagat tgaattaatg ctaaggaaag cattgtaatc cttgtgacca caccgatgga
                                                                        840
gatacagaaa aagttaacga ctggattcta tcttcatttt agacttttgg tctgtgggcc
                                                                        900
atttaacctg gatgccacca ttttatgggg ataatgatgc ttaccatggt taatgttttg
                                                                        960
gaagagettt ttatttatag cattgtttac teagteaagt teaceatgge egtaateett
                                                                       1020
ctaagggaaa cactaaagtt gttgtagtct ccacttcagt cagaaactga tgtttcagct
                                                                       1080
agycacagtg gtacatgcct gtaatcccag ctacttggga ggctgaggtg ggaggatcac
                                                                       1140
ttgaactcag gagtttgaga gcagccaggg caacacagcg agaccctgtc tcaaaaaaaa
                                                                       1200
                                                                       1217
aaaaaaaaa aactcga
 <210> 32
 <211> 765
 <212> DNA
 <213> Homo sapiens
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                                                                          60
 ccacgcgtcc ggtgaggtct catgtctgct tatgcggtgg ctcgctgctc agaacaggga
                                                                         120
 accattggag atactcatta ctctttgaag gcttacagtg gaatgaattc aaatacgact
 tatttgagga attgaagttg actttatgga gctgataaga atcttcttgg agaaaaaaag
                                                                         180
                                                                         240
 actggtactt ctgaattaac caaaatcaca gtattctgaa gatgattcta caaagcctgc
 tgtttctaca aaggetgetg atgattteta caaageetge tgtagtgttg etgtggeete
                                                                         300
 tgcttaaaaa agtagaaaac acattgatgc agcatgttca ccccaacctc cctgcctaaa
                                                                         360
 ggctcaggga ccatcttgga agaggaaggc gcgtgagatt gtaagagccg aattaggggg
                                                                         420
 atggagtgtg gagaataagg acacttcatc ttggatgctc acctgccaaa ttgacttctg
                                                                         480
 atgaaagcca gctccagaaa tgtgcctaca gttactactt tcacctaaac cctgccctta
                                                                         540
 gtcaaatect tetettette taageaatea aetteaatte ettgtataae eeacagtata
                                                                         600
                                                                         660
 aaagggcttt tataccattc tatcctattg catgtaagcc ttgggtctgg gaggtaacag
                                                                         720
 tgtgggattc caccatctca tctccctgcc acccaaacat gcctgctctt ctttaagcaa
                                                                         765
 tattaaatgt ttgtacttca gaaaaaaaaa aaaaaaaggg cggcc
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<210> 33 <211> 752 <212> DNA

<213> Homo sapiens

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                                                                        60
                                                                        120
ticatattac agotettact taaattigac caagocagga tatatotigtt aggocacatt
                                                                        180
catttaqqqa tcatgttttc caaagcaggt ttgggcaaaa ttaatccaca ggactgaaag
gtatacatet gtgagttttg tteteaette eaeetetaat ttgaagaaca etttaattga
                                                                        240
cacagaatan attteacata tttaacetet acaataagtt etganacatt ttecatgaaa
                                                                        300
caaaccatcg ctatattcaa gataatgaac ctatctatca tactcccaaa ttccttctkg
                                                                        360
catetttgta attteteact etteettete ecteteeceg teccatecea accaetgate
                                                                        420
tgeteaggea actaecaate tietttetgt eactatagat taatttgeat tittaaagaa
                                                                        480
attlacatac atggaaccat acateateta tgetttgrag tatgaeteet gteacteagt
                                                                        540
acastrattt tgagattoat tratgttawt gratgtatoa atagttoato cortttattg
                                                                        600
gtaagtaaca tttttttgta taggtatacc atgatttgtt gatgaacaaa tttacctgtt
                                                                        660
gatgaacatt tacgttgtta ccaagatttt tgctattgaa aataaagttt ttatgaatat
                                                                        720
                                                                        752
ttatatatat aaaaaaaaaa aaaaaaactc ga
<210> 34
<211> 2265
<212> DNA
<213> Homo sapiens
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 <222> (300)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (2162)
 <223> n equals a,t,g, or c
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 <222> (2258)
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                                                                          60
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 gcacctaccc agaggagaag gtagatttgg agtaagccgc cgtcgacata attcctctga
                                                                         120
 tggttttttt aacaatggte eectaegaae tgeaggagat tettggeaee agseeteeet
                                                                         1.80
 gttccgccat gattctgtgg actctggtgt ctctaaggga gcatatgctg gaatcacagg
                                                                         240
                                                                         300
 gaacccatct ggttggcata gctcttcccg aggtcatgat ggcatgagcc aacgtakggn
 aggtggcaca gggaaccatc gccattggaa tggcagette caeteeegga aagggtgtge
                                                                         360
  ttttcaggaa aagccaccta tggagattag ggaagaaaag aaagaagaca aggtggaaaa
                                                                         420
 gttgcagttt gaagaggagg actttccttc cttgaatcca gaagctggca aacagcatca
                                                                          480
  gccatgcaga cctattggga caccttctgg agtatgggaa aacccgccta gtgccaagca
                                                                          540
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| caacagcaca cotqaaccaa aggaaaatgg ggaggaaggo tgtcatcaaa atggtottyo          | 1030         |
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| attraaaget atgggttgge aggaatatee tgaaaatgat gagaattgee tteeeeleae          | 1200         |
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| capaggaggg titgaggagt cagagaggga aaccagtagg agtgaaacat cagalyacya          | 1330         |
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| tragggagta tacaaaaqaa ategttettt teettitett atgitigitga ataciicatt         | 1500         |
| casaagggaa ataatcatat cccaaagaga gagcaattgg cttgttttgc ttttgttatt          | 1560         |
| gricticeer gitatetget tiataqagag aagittgigi ggigggacag attititiada         | 1620         |
| cacactcava cacacacaca catacacacc cagtatatat ggggcgatgc acaggtagga          | 1680         |
| gotagoagta cagagaaqaq qaqacactgg totgoagcaa cagottotad taccagcot           | 1740         |
| rgggggacte acceptga teaaqeaate attgteaatg acaaagtgae tattgaaqui            | 1800         |
| araattgtat taaattaatg ctaataattt ggatatttta tittaittit ggdigdiegg          | 1860         |
| graacttrag cocttaacca agcatatgtg ggtttttttt gttgttttt tttgttttt            | 1920         |
| fittettitt eetittiggg taeagetgta aaatattigg atataggaaa igiligigua          | 1980         |
| trottgcago ottgatatto agggtggatt gtaaaatata aatttttgtg agallicaaa          | 2040         |
| gattaagatt attitgataa cattatitac agatttaaaa gaigiggita teacaayiet          | 2100<br>2160 |
| cgaggggaa actactgcat aaaataacta acttggaata aatattttgc atcagtilgg           | 2220         |
| anaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa                                   | 2265         |
| aaaaaaaaa aaaaaaaaa aaaaaaaaag gggggggncc ccccn                            | 2200         |
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| 400. 35  |              |
| <400> 35 gaatteggea egagetgetg tggggeeaaa egeateatga aggaagetet ceaetgggee | 60           |
| cttttcagca tgcaagccac gggccacgtg ctgcttcacc tcctgttacc tgcagcagct          | 120          |
| cottogatgoo acagaggacg ggcatcocco caagggcaag gcotcatcoc toatcocgac         | 180          |
| ctgtctgaag atactgcagt gaaagcccaa gccctagctt tccccagtga aggactagac          | 240          |
| taggggccc acgctcaact ggtagtggcc acaagcctgg cagctgtaga gccgctaacc           | 300-         |
| tecegacaee teceteacea caeaaggaeee tgagtgagga ggaggggetg gaaacetggg         | 360          |
| rtgggttggc caaaggagaa cctcaggctc ctggcctggc                                | 420          |
| gragettage ccatecagae tggteetgaa gretgteeet ccattggeat gaagtetgee          | 480          |
| cctcagcagt ccggcctcac aggctgtact ttcatggtgc tctctacctt ctggcccca           | 540          |
| toccagaaca thogtgagtg aathogoaag catachagca tghgatatha gggagthigo          | 600          |
| aataaattat tgatgctgaa aaaaaaaaaa aaaaaaaact cga                            | 643          |
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| cccagcccag tcaagagcta ccggggctgg ctagtcatgg gggagcccag tagagaggag          | 120          |
| tataaaatcc agtcctttga tgcagagacc cagcagctgc tgaagacagc actcaaagat          |              |
| tataaaatcc aqtcctttga tgcagagacc cagcagctgc cgaagacage uctoudays -         | 180          |

240

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 gccatatttt acacaaaatc atgttgtggg agccctcgtc ccccctcctg cccgctctac
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 caggiccett ageacetgic eccetgeetg tetecaging gaaggiagee tiggeeaggeg
                                                                         360-
 gggcctcccc ttcgacgacc aggcctcggt cacaacggac gtgacatgct gcttttttta
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                                                                         600
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                                                                         780
  aaggatetgt caeggaagge gteettttte ettgtageta aegttaggee tgagtagete
                                                                         840
  coetcoatco tigitagacgo tocagiocot actacigiga eggeatitico atecetecco
                                                                         900
  tgcccgggaa gggaccttgc agggacctct ccctccaaaa aaagaaaaaa agaaaaaraa
                                                                         960
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<213> Homo sapiens

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                                                                     240
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                                                                     300
cettaaaace tgttaateag ttaaaggogg ggaacaetgg tgeetttttt tttttttt
                                                                      360
taacttetta accaagggae agtgaagaet tttaagttag atetgatttt agaattgeag
                                                                      420
ttgaggtagt gcctagtgtg tgaatttgag gtcattttct aaactggccg ggcacagtgg
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                                                                      608
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 180
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                                                                       300
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                                                                       720
                                                                       780
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                                                                        120
gggctggttc ggacgtgggt cgaggctgta gcaggactcc aggaagatgt taccgagtac
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ttcagtgaat teettagtge aggggaaegg agtettgaat teeagggatg eggeaagaea
                                                                        240
cacageegga gegaaaeget acaaatatet gagaaggett tteegettte ggeaaatgga
                                                                        300
ctttgaattt gctgcctggc agatgctcta cctgttcaca tccccacaga gagtttacag
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aaattttcat tatcgaaaac agacgaagga ccagtgggcc agagatgacc ctgctttctt
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 acttcaccca tactctctgt tctttctata agtacagagt gaaataaaaa gtgagaagaa
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  atgcaaattt tgcctttgtt ttctgtcacc ttccaacccc tgagcacttc tagtcagata
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                                                                         780
                                                                         840
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 aatcacagge geetggagag cageegggea eegeeteeag ggaeetgeeg getteeetea
                                                                        1080
 gteetecagg ggeecageae tetteettta ggeectgtga gegteeettg teaggataca
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| cagaggaaga ggtggaagag teeteaceae tgeaagagee accaageeag geageaggea  |      |
| grandered recagaceet aaggeetate agettetate ageergeage geergeerge   | 180  |
| tgggeetgtt ggesgeeace aacgegetga chaatggegt getgeetgee gtgeagaget  | 240  |
| - Ettentant accorangga egtetggeet accacetgge tgtggegetg ggedgegetg   | 300  |
| ccaatcccct ggcctgcttc ctggccatgg gtgtgctgtg caggtccttg gcagggctgg  | 360  |
| geggeetete Letgetgage gtgttetgtg ggggetacet gatggegetg geagteetga  | 410  |
| geggeetete tetgetgyge gegeetege gaggarangt erteatagta etategtggg   | 400  |
| gedection teeggogatus solutions against cottog etgeteggg gedectiges gedectiget gedectige | 540  |
| tgctgtgtst tggcgtgtte tectacqtqa aggtggcage cagetecetg etgcatggcg  | 600  |
| ggggccggcc ggcattgctg gcagccggcg tgqccatcca ggtgggctct ctgctcggcg  | 660  |
| ctgtigetat gttecceccg accageatet atcaegtgtt ceacageaga aaggaetgtg  | 730  |
| cagacoccto toactoctoa quotigggeag gtiggggacco egeleeleaa ealeeligietti   | 780  |
| taggtgaatg ctgccaccat gcctgagtgc ctgcagccca ggaggccege deadbygda   | 840  |
| netgatagac acctacacac tocataggag atcotggott tocayygtyy geddyggedd  | 900  |
| grandament tomagecage gaccagtege ggetetaggy taageceete agectaggan  |      |
| ctacatgtgg titgcgtaat aaaacatttg tatttaaaaa aaaaaaaaa aaraattact   | 960  |
|  | 965  |
| cggtc  |      |
|  |      |
|  |      |
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|  |      |
| <400> 46   | 60   |
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| ctgattctgt aggtctgggg tttccagagt ccgcggtttt gctaagaagc cgcagtgatg  | 180  |
| throughout the technique the transfer of the technique the transfer of the technique t | 240  |
| gatagatca actagaaget ggacaacgtg ctgatgccta gtcccagaat ctggcccag  | 300  |
| at an at case canadagate tacetetate addagtgagg gradeacete etcaetagg  | 360  |
| nathtataag chaqqaaqqa tatqaatqco ataqtaacca gaacciyiga geelgigaag  | 420  |
| agatetacag totacacoca oggotgtggc tgtgtgaggt ttgtcacaaa cassassag-  | 480  |
| engtester gacaacaag gcaggcgcc cggcaggaag aggagaacte adteegeagg   | 540  |
| recentrata gradadad cedeetgge tacceceta graceated georgation   |      |
| garage cota actage cota toto etto a atage cota type cota actage cota total   | 600  |
| catagagaca actactataa catcoctatt cottaaagtg cygygtteet cyclyddia   | 660  |
| testacetaa etggcaceet gtgcaaacet gctgcagaga acagegeete gggodgogog  | 720  |
| atagteetee agtteaceaa cagtaaaaat ggteteaatg gggagagaaa aaaaaaaaaa  | 780  |
|  | 791- |
| aaaaactcgt a   |      |
|  |      |
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| tacgaaaatc acatattttt ggccttgttc ctctgagaac aaaaacatgt aataagagat  | 180  |
| acctgettte atettttgea atgaatagaa tacteteeta ettagaaaca ggetttttet  | 240  |
| agrigaçaçi traffittic citacciatq aattqcatgt gcclligaty aaddcddegd  | 300  |
| Tabagagata tacaacaata catataataa actgaatgca acttagadgt ggccaccete  | 360  |
|  | 420  |
| trattteact trattatt agratetaca gicteteatt ettillete aaluatate  | 480  |
| attratata aattratat toagocatga cictattatt toagogacatga cattatt   |      |
| togaggattg ataccatgaa aaaaggttat ctagtagttt tgagtgaaga tacgaggcac  | 540  |
|  |      |

| accttcaata ecaataagaa ggtatacaac aaaggtetaa tgaaqaaaaa tateteattt<br>tgaaggtage acatagettt caactgaetg ggeetgttat ggtetttget gtgtttgtta<br>teacagtate taatagtgaa gtggtaatta etttetttag tagaaattee aaqatetaaa<br>ttggtacaca tataaatatr tgacaacaaa aaaaaaaaa aaaaactega   | 600<br>660<br>720<br>779  |
|--|---|
| <210> 48 <211> 875 <212> DNA <213> Homo sapiens  |   |
| gaatteggea egagetgggt ettetagaag acqaaqatet atecaaaate aagaageett ggttacaage tetteegggee egggtaggag teggeatgge ettattgaa ggaaaactea agattetgaa aagaaageaat teetetgage gagaaageaat teetetgage aatgaagea agattetgt aatgagea agattetgt aatgageae teaaaacte agatteegaagaagetgaage ggagaaage egggtaggag teaaaacee agttetgagaa actetaatat agatteega aatgagatet eagaggeteeat ggagaacagge ggagaaaget tacaaacteegaagetgaage | 60<br>120<br>180<br>240<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>875 |
| <210> 49 <211> 614 <212> DNA <213> Homo sapiens  |   |
| <pre>&lt;400&gt; 49 ggtcgaccca cgcgtccgac ctcccctcc tgggctaaag tggttctcag ctcactgcaa ggtcgaccca cgcgtccaag tggtctcgtg cctcagcctc gagagcgcca ccaggcctgg ctaattttgc atgttttgta gaggcagggt tctaccatgt tggccaggct ggtctcagac tcttgataaa ataaatgatt aaattgtgtta aaatgcaaaa gagggaaaga atgtttttac ttcattggca gtctgggtaa aaaattcata gaagacagaa ttatttagct tttattttac tcattggca gtctgggtaa aaaattcata gaagacagaa ttacaggttg ctagtcttgg cctgaaactt ttagctgtca caactggggg atgctgg taaaaaaattcata gaagacagaa ttacaggttg aaggttaaa caaataatat taaagctctt tttttatatt aatgtggaaa aatgttattt tggttcccat gagaaactgc tactatttga aalttaaaaa aaaaaaaaaa aaaaaaagggc ggcc</pre>  | 60<br>120<br>180-<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>614                     |
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<220> <221> SITE

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gecagaatat accaaacgaq atggcagget caatetggee tetaggetae etagetaett
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tgtaaggcct gatctgggcc ccaagatgta caacgcctat ggtatgaggg agaggctaaa
                                                                      240
attgctcttt tgggggactg ttgttcttat ttcaactata gaaggatatc tgtggtcaat
                                                                      300
gtcaggtata gagatgattg caggcaagtg ctggagaagt gaatagratc caaggtqgtc
                                                                      360
ttgaatatgt ttgcttttgt catattggtt ttcataacat ccatgtgggc ccayaccata
                                                                      420
agettacatg tetecagtag tgaggaagtt teetgttaag aactetacce aaggageeat
                                                                      480
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ctgggccgtc cgttta
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                                                                      120
 tegeogttet tgttegeett ggaacegeet ttgceggaet tgaeegaete ageategatg
                                                                      180
 tecgteateg tagategtag atetegagge tetgatacea attgttgget tttaaacegt
                                                                       240
 agatcaaaac acccaggagc accacgtatg tgtacgtgca aagctaactc gaacaagtac
                                                                       300
 actagcaget tgacegatta gecettgtae acaegtatgt geaactaget agagaettge
                                                                       360
 gtatgaatac ggttcagccg actagcttcg gttgattgga tcaatcacgc ggcaatggat
                                                                       420
 caactcggst ctctcaacaa gaacgtaaaa mgcaargcac tgaatcgttg atggcacagg
                                                                       480
 540
 caccaccett agggtgeett ttatacacat cecacaaggg actatgggeg gtgatgaaga
                                                                       600
 tgaagattat totoogaaco otootagtgt ggcacgcaat cacggacgac gacgtcgatg
                                                                       660
 acgaetecga egaaggtgee atggeegeea tageeeggta catgeeggat teegtgetga
                                                                       720
                                                                       780
 tgacattggc ggagttcgag acagcaagag aggcgtggaa cgcactcaag aagatgagga
                                                                       840
 toggagaaga togogtoaco aaggottgga cacaagtgot gaaacgocaa tttcacaagt
 tgcacatgga ggaaactgaa tcggtgaacg actacgccat gtgtcttact actttggtgg
                                                                       900
                                                                       960
 gagagttccg cgcgcttggt gcaaagctcg atgagaccga gattgtggag aaaattttca
                                                                      1003
 gttcagtgac tgacaaattc acgtacatca tcggcacgct cga
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  <221> SITE
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  <223> n equals a,t,g, or c
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                                                                  120
180
augesttggi etttggaggg acagaaagce accagecaat ggagaacaaa gagatgttte
                                                                  240
cettteettt ettteacett gteattetgg gttteettet getteactet treetteece
                                                                  300
cttaaaagtg gtatteetgg ttggtetgte tgtetgteet tgteettgtg gtgateetgg
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                                                                  420
ggaggateta accaegeetg gtggtgagga agetgaattt ecaggeetge gteecatgta
                                                                  480
geotetecat gaactgeaga aggeatgtte tgeatggtta ceagtaagtg getecetete
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acceptettea tregreaaate agageaaact traggreette gerecattet acaeteract
                                                                  600
tgctctgctc ccctccctcc aaccagggtt catgtcagtg cacaccccat gtgccctggc
                                                                  660
gaagetggtg etgtgagtga tgttteecat acaaeteagg gatgeeaggt ggettaeeet
                                                                  720
gagatagtca ttttgggcac ataacagtgt aggaatgaaa catggatttc attgatattt
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                                                                   120
caceteagee teceaagttg etgggattae cagagaagag getgaaggge aaggagggaa
                                                                   180
aggaattggt teccaggtee atggacetet tgtgaageee eeattgetgt ggggtetgag
                                                                   240
 gaaacacaga ggaggtgtca gctgctctgc ctgccccac tcccctgcca acaacgtagt
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 aacetetgtg cetaacetet gagecetgge etceaaceet gggagggagg taettatgtt
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 420
 tgtctgtctc cagagcccag gcccccagtc aacaacttgc caggtgcccc tctccaggcc
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 teggettete cacetgtggg teaagageae caggettgtt etagagetat etteteagae
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                                                                    120
 ctattattgc aaggactaaa attatgaata tgtgctggca aataccaaac tttatattaa
                                                                    180
                                                                    240
 tacaagtgtc atcagaatat gtacatatat taatagtaat tgttaccaaa acaccagggg
 ttcaatctgg gtcctgctgc tcactgcaca gaaagccaat gcctgagaca acaagtgttg
                                                                    300
 ccaaggaaga aggettaatt gggtgetgea geegaggaga tgggagetea gteteaaate
                                                                    360
 catctctctg acagaccaaa actggctata tagcarggaa gaaatgtaat catgtgtggg
                                                                    420
```

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aaaanergga acteagaaqq ggettggaag caateatqtt gaateagegt ceacatttta
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gtcatttcct gaggaaggat ctcagataaa acaaatafaa gtttcaaatg ttaagaccag
                                                                       600
aaagttcaat fictatgitt ätttattott tittitaaaa aaaaaagcta taigggacig
                                                                       660
ttgggttggt ttcataatgg ctgagtactt tgaaggttct gtggttgcat gaatggagaa
                                                                       720
gatagagtga tgggtggqqa cittaaaata ggatgatcca ggaatgccct qaagtagaga
                                                                       780
cttgtaagaa tgagaaatag caagttatgc gggtggcata gaaaaagctt ccagattgaa
                                                                       840
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                                                                        900
                                                                        933
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                                                                        120
                                                                        180
 ctgccctttg cttgggcccc tctaccagta tgtccagcat gtgcccgggg gccctcagct
 ccectggggc ccagcccacc caagacacag ctcttggtcg tgaacatgaa gatgagccaa
                                                                         240
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                                                                         300
 tettttttat ttaataetga ggaaceggag tqgaggggte etgeeggget geagtgaeee
                                                                         360
 tgagggaagt caggagagcc ctgggctgca gaagagtccc cccacaggct ccgaagcaag
                                                                         420
 cttgtcctgg tgcattcaga ctgctcacag caggetttgg gccctcactc tccagatccc
                                                                         480
 agagageeet eeagggetee eagetetegg geeagtgeee amgteetega aggggggeeg
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                                                                          180
  getteatgag caaageeact geageatege aeggtgtate tetgageaca getgaettga
  cagaaggact caactgtcca cattaccgar gactgaggta tacggaatgg titctgtttt
                                                                          240
                                                                          300
  gettetteaa ggaggggaae tgaaacccaa etaaatecaa ggtgeetett eeaaegeetg
                                                                          360
  taactaaact tcaagcatca cagecccaac acctgctgat ggcaccattt taactgaggt
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  ccatcccgca agettcccga ctgtccacac tggctctctc tactcctgtg caccaaagar
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  aggetgagge atgagaaceg ettgaaceeg ggaggeagag gttgeagtga geegagaegg
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  egecaetgea etecageetg ggagacagag egagaeteta aaaaataaat aaataaatta
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  aataaataaa taaataaaat taaaaagata gtgtaggcta caaacctcag gaagaaaata
                                                                          660
                                                                          720
  ccagcatgae ttcagaatag tcagammtaa tggtgtataa agtteteeeg geteetetee
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tggtgatggg gtgtgtgcaa ggcccgggag agggttgtag tgggaagatg gggaagaagc
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cacgcccctg gccactagtt tcttattcga ttactcatct gragagaaat ttgagacgca
                                                                        240
teacetgace cateegteaa ttegeatetg geatetaaaa geaceagagt eagtgetggg
                                                                         300
gaaaacacta tttaaaaaaaa ttcccagttt aacctcatta agcctctgtt ttcccatttg
                                                                         360
taaactacag acagactgga gacttgtaag agataaatct aattctttca tagacattaa
                                                                         420
tgatccttga aaaaggatca tttgagggac atggagattg gtttctactg tttctgttgt
                                                                         480
tactaacact octootttoc caaggoottt agaaaggggt gagototoca toacagaaag
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tattcagata ggcttccagg aattttttgg gaaaatgttc ctgctttgag taaqacacag
                                                                         600
gaetagatea gegtttggea aactatgget egtgggetaa atteegeece teteetgtgt
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  <220>
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  ttccacaaac tcttcattgt ctactgacaa ccttacttct atctttactg agaccaaaaa
                                                                          120
  aaaaaatcag atgagttatg cccatcacgt caccgtattc ccaaactacc tgcctctgtg
                                                                           180
                                                                           240
  cacaccacct cactgeetge tgeagttact gteeagggee agegeetetg eccatgtact
                                                                           300
  ggageetgte cetecaceet tttcaageat gttactetat caaataaata teeetttete
                                                                           360
  tritigicatia tragititige tatricticity triggererae cagractati accratigeta
  tattagettt taaaaaatte teteaatete acatttatet eeaaegttta eateattett
                                                                           420
                                                                           480
  ttgctgcact ttgtagaaaa atattttgaa ttttctgtat clatttctac ttccttactt
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  cccatgtttt cttgaactca ctcgangggg gggccgggan ccaattcggc c
   <110> 59
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                                                                             6.0
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|--|-----|
| ctagatocca tictitotto toccollett circleged is<br>ctgtaccgta taaagatgot atattitoto coatotttaa aaaagaaaaa gtototitta<br>ctgtaccgta taaagatgot atattitoto coatotttaa aaaaagaaaaa agaaaaaaaaa  | 180 |
|  | 240 |
| accontants tooctocage tactadely at white to a superstance and superstance and superstance accordance and superstance accordance and superstance accordance accordance.   | 300 |
| auguststyt gigigriffic ittiligiling eletigiouss and garagerater gattgigget cactgeaged  | 360 |
| augustigus statisticance aggstigus statististis satististististististististististististist   | 420 |
|  | 480 |
|  | 540 |
|  | 600 |
|  | 660 |
|  | 720 |
|  | 780 |
|  | 840 |
| trototgito cacagitatot ggagoorigg corgadyare and the total gacotcagit to the total control of the total control of the total cagainst the total ca | 852 |
| teettteetg eg  |     |
| [66666666]   |     |
|  |     |
| <210> 60   |     |
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|  | 120 |
|  | 180 |
|  | 240 |
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|  | 360 |
|  | 420 |
|  | 480 |
| ctttccattc ccagattctt tigttgttgt tegetgagca cagtggctca cacctgtaat tgacacatga gagtatggag ttttcccaaag ctgctgagca cagtggctca cacctgtaat   | 540 |
|  | 600 |
| cctagcactt tgtggggatg aggcgggatg attacted of agagtgagat cctgtcaaaa gmgagctgtg attgtgccac tgcattctag cctgggcaac agagtgagat cctgtcaaaa   | 660 |
| gmgagetgtg attgtgccae tgcattetag tetgggcaas mg g g g   | 680 |
| aaaaaaaaa aaaaactcga   |     |
|  |     |
|  |     |
| <210> 61   | -   |
| <211> 894  |     |
| <212> DNA  |     |
| <213> Homo sapiens   |     |
|  |     |
| <400> 61   | 60  |
| <400> 61 togaggttag actgcataga aaacaatttc agatttcctg gaggctgcat aaaatttaac togaggttag actgcataga aaacaatttc agatttcctg agcaaaatat  | 120 |
|  | 180 |
|  | 240 |
|  | 300 |
|  | 360 |
|  | 420 |
|  | 480 |
|  | 540 |
|  | 600 |
| L TEFFOOD AND FORMALL ALACTOR TO THE TOTAL | 660 |
|  | 720 |
|  | 780 |
| gtottgocaa attgagtttg tidagdaget tagaaababb 55 caaacaccat tggttagttt caagcatatt tratttaaaa aatagtcaga caacatottt caaacaccat tggttagttt   | 100 |
| Caagcacacc   |     |
|  |     |

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tcatacaaaa tgcaagtttt atcaqggtat atttttattq taaacttttc aaaattattt
                                                                     840
                                                                     894
ttaattatgt gggcattiit tatgictaac titatiigca cicgigooga atto
<210> 62
<211> 691
<212> DNA
<213> Homo sapiens
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                                                                      120
aaagaaaagc aagtatatca tatttcaaaa atcaaagagg aatacagtat attgatttgt
                                                                      180
cttotgatag tgaagatgtc gtttccccaa attgctccaa tacagttcaa gagaaaacat
                                                                      240
tcaacaaaga tacagtgatt atagtttctg agccatctga agatgaagag tcccaaggec
                                                                      300
ttoctaccat ggcacgtaga aatgatgata tttcagaact ggaagacctt tcggaattgg
                                                                      360
aagaccttaa agatgctaaa citcagacti tgaaggaact tittccacaa agaagtgaca
                                                                      420
atgatttact taaggttata ttcattggtt attgtagctg taatgatgat aaaatctctc
                                                                      480
ctgcattcag tgctatagtt agtagtggat agtcattttt ctaaagatat cttacgtttg
                                                                      540
aagatattaa ctattaaatc taaaggaagt aaatgccaga catttattia ttgaaagtct
                                                                      600
taacttttta atagatgagg ttatttattt gtaaatagtg cagtaattaa agccttaata
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                                                                      691
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 <223> n equals a,t,g, or c
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                                                                       120
 cctggtttgt ggggcatgtg ggatcaaaga cccactaaag gaacacagga ttttcagctc
                                                                       180
 240
 geteettete caageattgg tacatgtett tgtgetagtt aagettgagt acattgtgat
                                                                       300
                                                                       360
 ttcactagat cacactccca atttcaagkk cagtgtgaag aatatagagg ttctggttgg
                                                                       420
  totagecttg gecaegtatg agtagacace eccagttnea aaggteaact ecaettetea
  ctagaattaa aaagctttac tocaaatgta gttaaaacag cocaatatot tootottata
                                                                       480
  agcagtaatt aaactffagt gtggataaga ttcatctggt ttgcttactt gaaaatgcag
                                                                       540
  atetttgget caacetetag aagatgggac agagecagag tggggttgga tggggttgag
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  aaatctgcat ttcaacagta gtccacaggt gactctatgc agaccctgga aaacactcta
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  tttaagggct caccacagcc agggaccata ttccaactgt cacttttcta ggtctcattc
                                                                        720
  tcattatttg ttccaagact ctctcttatt tttgcaaatt taatttaaaa gtatgagcat
                                                                        780
  ttcctgaatg taaccagcca ctctaagcca gagctgacct atgagggaca catacgtggc
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                                                                        891
  caaggctaga ccaaccagaa cctctatatt cttcacactg aaccggcacg a
```

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<220>
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geggeteaga gggaaggaga gaettgeeta aetteaggge aagetaaege ttgattteaa
                                                                      120
ettgataaat ttetgagtat geagligggtg cacatageag agacaggtaa tgagaagttt
                                                                      180
tettttttcc ttttctttt ttgtgggggg tygggacaga gtctcactct gtcacccagg
                                                                      240
                                                                      300
360
caagegatte tigigeetee geeteetgag cagetggeae taeaggigea egeeameaeg
ctgggctaag ttttgtattt tagtagggat ggggtttcac catgttctac gtttcaccat
                                                                      420
gttggccagg ctggtcttgg actcctggcc tgaagtgatc tgcctgccnt cagtgtccca
                                                                      480
                                                                      540
aaagtgttgg gattacagge gtgagecace geacteggee gagaagtttt tetgattaaa
aaaaatttta aggcacacac ttcagacagt ggctgtgaag gaaccctgat gtgtatctaa
                                                                      600
actgtcgcct cgtgcacatc accccattac ttactctgtg ctaagtgctg tcatgcatta
                                                                       660
 catcattact cettagaaca ggeetatgag gtggagtetg cattaggeee attttggaca
                                                                       720
                                                                       780
 aggacaccaa tagtgtggga ggtggtgtac cttgcccaag cccccagcag gtaagtggtg
 gtggggatta ggacccaggt cacttgagtc catatectgg getettagtc ccactetgec
                                                                       840
 t.ggctgcctg ctgctccatg aagccaaccc tggacctaga cctggacctg gatcgtcata
                                                                       900
 geocagatee etgtgtgett eccaggetge ettgtggeag gtggatggtg eccetega
                                                                       958
 <210> 65
 <211> 802
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
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  <400> 65
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                                                                        60
                                                                        120
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  tgttttatga tgttcagggt cccagccatt cctcggaaat gtgttttttt gttttttt
                                                                        180
  ttgtttgttt gtttttgttt ttgatgaatg agtctaaagg ctgagtggct atcaaacaat
                                                                        240
                                                                        300
  tetttttggt ttacattgta ttatgaaaat aatataaaaa eeetgtgtae ntttettgtt
  tteettteta tagttttggg gaacaggtgg gtttttgkta eetggataag tetttagtgg
                                                                        360
  taatttotga gattttggtg tgcccatcac cocycogtgt actttaaaat gagtaagttg
                                                                        420
  tgaaaatgtc aactagtttg ctatttagag ggtcctcata aagtaacaaa atgatacata
                                                                        480
  acacatttgc acagcaagtc ctcacttaga gttgtagata tgttcttgaa aactgcgact
                                                                        540
                                                                        600
  tcaagtgaaa caacatataa caaaactaat tttaccatag gctggttgac acaaacaaga
  gettagttee taccacacat tactggteat aaaaacatga ecaaatetet aactaaagae
                                                                        660
  caaaagactt ctaataataa acatcgagat aaatgtgagc tatacctacc tttaagaaag
                                                                        720
  attagtgtaa acaagtaagg taatttactc agttattcta gttcaggact gtgggtagcc
                                                                        780
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                                                                    120
atttttactt aaaggaaaat gctgctattt gtgatgaaat tgctcgtctt gaggaaaaat
                                                                    180
ttottaaago aaaagaagaa agaaggtgag otggottoat tttgtgttoa goatoacott
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tgggattgat gcgtatcgca cagccccttg gccacttgat caagcacaga gaaacttaca
                                                                    360
gootgaggea tiggigeetg cacacccaag tiatgitggg ccatggegat gagacagete
                                                                    420
ctotactoat otttotgaaa aagocatott gocacatota ataaataato ttaotaagat
                                                                    480
tatttaatct tatggcccaa ttataaaagc caagtgataa aagcaactgc ctctcgttct
                                                                    540
acaaatattt attetgtaeg taetattetg tgeaaageae aatgggtata tataeatgtg
                                                                    600
taaataatgt gcctttcaga agcctaacac cgtccaacat caaggtagag gaaccgtcca
                                                                    660
gatgcaagag ataagctaca gttcttatcc ttggcctctt gaagtattga ttatcctcca
                                                                    720
gggctttatg attcataggg cctaataaga acctttcttt tatgagtata gtaatctttg
                                                                    780
                                                                    840
tatataattc tggcttttcc cagtacttga gtaaaatact gaattgagac aatacggaag
                                                                    900
ttcatttctc tgctcctttc cttcctgatc tcaggtactt gctaaagaag ctcctccagc
 ttcaggctct aactgaaggg gaagtacagg ctgcagctcc ttcccacagt tccagtttgc
                                                                    960
 ccctgactta tggtgtggcc agctctgtgg gaactataca gggagctggg cctatttcag
                                                                    1020
 1080
                                                                    1092
 aaaaaactcg aa
 <:10> 67
 <211> 734
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 atgtgctcat tggccattta tagatctact ttagagaaat gtctattcaa gtcctttgcc
                                                                      1.20
 cattgttttg ttttgcttca ttttttattt taggttcaag gggtgaatgt gcaggttttt
                                                                      180
                                                                      240
  acacgcatgt attgcaagat cctaqagctt gggcttctaa tqatcctgcc acccaagtag
  tgaacatagt acccaatagg gagttttcaa cgcttgccct ccttctccct ccccactttt
                                                                      300
  ggaatccctg gtgtccactg ttcccgtgtt gtgccatgtg tccccagtgt tgagctccca
                                                                      360
  cttatgagtg agaacatgtg gtttttggtt tctgtntctg cattaattca cttaggataa
                                                                      420
                                                                      480
  tggccccag ctgcatctat gttgccacat tgtacatgat ttcattcctt tttctggctg
  540
  ctcactctgt cacttaggct gaagtgcagt gacatgatca cagetcattg cageetcaac
                                                                      600
  tteecagget caagcaatee eectatetea geeteetgag tagetgggae tgeaggtgca
                                                                      660
  taccaccaca cctggctaat ttttgtattt ttggtagaga cgaggtttca tcatgttgcc
                                                                      720
                                                                      734
  caggctggtc tcga
```

```
<21€→ 68
<211 - 706
<212 · DNA
<21% Homo sapiens
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<400> 68
                                                                         60
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taacaaacaa gcacagagat aactaataac actacattta attttattcc cctttttaac
                                                                        180
tttttattta tttatatatt alagtgotat gtottgaaaa gttgttgtag ttattatttt
                                                                        240
gataggitta tottttagto titotacaca agatatgagi agittacaca ciacaattgo
                                                                        300
agtytcataa tattetgtgt ttgtctgtga gtwttgtacc ttcagacaat ttcttattge
                                                                        360
tecettttet tteagaatga agaaeteeet ttageattte ttatageata ggtetggtgt
                                                                        420
taalgaggte ceteagettt trgtttaeet gggaaaatet ttatttetet tteaegtttg
                                                                        480
aagtstattt ttactggatg tactattcta ggatgaaagt tttttccttc aacactttaa
                                                                        540
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                                                                        600
tgtgggaget catttgtatg ttatttgttt ettttetety actgeettet tttaagatte
                                                                        660
                                                                         706
tttetttate ettgacettt gggagtttga ttattaaatg eetega
 <210> 69
 <211> 436
 <212> DNA
 <213> Homo sapiens
 <400> 69
                                                                          60
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 gaggtecceg eggtyteegg teceetette eggaggegge tecaggtgtg eggeeaacae
                                                                         120
 aggtgaaagg gscggggccg cgggaggggc cggggcgctc cctggctgcc tgaatggccg
                                                                         180
 ggcggggtcg agggagagtc gcttcctcct gggtgggggg cactggccca acctgctgtg
                                                                         240
 gttgcaaatg gcccggccag ttaactgagc atctactgtt tgcagatcct acattgaggt
                                                                         300
 agecteeget eettteeegt cacgaetgee ttgeeetgtg gggeaggaaa ttattageaa
                                                                          360
 tgacaacaac accgaatctg acatcttaag cattctgcta agtaaactct tttttatttt
                                                                          420
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  <210> 70
  <211> 721
  <212> DNA
  <213> Homo sapiens
  <220>
  <221> SITE
  <222> (7)
  <223> n equals a,t,g, or c
  <220>
  <111> SITE
  <222> (644)
  <223> n equals a,t,g, or c
  <220>
   <221> SITE
   <222> (718)
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<223> n equals a,t,g, or c
<2220>
<221> SITE
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<223> n equals a,t,g, or c
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                                                                         60
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ctgggagtgg gtgagacgag actcggggcc tctacatctg agtgtccccc aaaccgagca
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gtcatgtcgc gagcaaacaa agaaatcatg ttacttcttc cagctgatgt tccacttgtt
                                                                        180
                                                                        240
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ctattcccca gagcaggaag tggtaggcag gggccaggaa tggattttaa aggcaaagtt
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ctcaqaccca gtgggaactc gaactggtaa actctcctca agctcccaag gacagaggat
                                                                        360
traggetett gttggetett gtccacagee acagaactea aggtetgaat etggaatete
                                                                        420
ttgacaggac agtaacataa acctctagag atggaqtttg agaaaggccc ccccttctgc
                                                                        48U
cagettgtga tttagaaaag tgeatteatt caataaaeat ttaetgagea egtaegggee
                                                                        540
aagtacggtt cttcacagaa gatttagggc ggaaaaggac agacaggagc ctttggccct
                                                                        600
                                                                        660
gaggtttcca ttctaggagg cctttaaatc tcagactctc agantaacag agactatgat
                                                                        720
tactcactat teetetggaa caegagecaa aagagagtge tgtcagatea agacaatnng
                                                                        721
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<211> 793
<212> DNA
<213> Homo sapiens
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                                                                        120
 ttaaattttt ttotacotca catcagatag agacaagoot cattgocato tooctgtaco
                                                                        190
 agaatgtgga atttttcttg ttcaaccagt atttgtgagt atggcttttt aaaatttctg
                                                                         240
                                                                         300
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                                                                         360
 ccaaccaagt gcaaaattaa atagaattet tgtgatatea ggggaaacaa aatateteee
                                                                         420
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 ctgtttctcc tgatgttttc tctctttctg gcaaaaaagr atgttattgc atattacaaa
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                                                                         540-
                                                                         600
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 gggtgtgtca cactcctact taaaatcttc aatgacttta tatttctatt atcataaaat
                                                                         €60
                                                                         720
 tocatotoot toatattaca taaaaggaaa tootacottt caagtotaac ootttgotat
                                                                         780
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 tgtccaggca tttgttttca agtgccaagc ctggggaccc aggaggagaa gggaaggact
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 tecetgggat tectecaaac tgtetecett gageageact agaeteacta eetgeteeee
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300
acctoccace teaggaaggg gactgeaggg tacacaggag getgegeeet ggacaccagg
                                                                     360
соссадосос ассаваесот садтосссая адосссадае сетдаастту ссаддассат
                                                                     420
gcagyctggg ctactgtggg tcttggcaqa accagcaacc aatggagggc gagaaggaag
                                                                     480
gagatotota acattiticae agaacaaaco acqeaggaac ecaagaaagg etgaagtict
                                                                     540
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                                                                     660
ggaaaggcta ggagggagac gggtggctte tggctecagt gagaceegag getaletget
gcagacecca gattgcagge caeggteeet gtecagtgge agggeaccag cetacettge
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<210 > 73
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<212> DNA
<213> Homo sapiens
<400> 73
                                                                      60
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ggagaggatg geactgtgec etgtgettga tgtacacaca catttggggt geatcatetg
                                                                     180
                                                                     240
tgtggcctgc cagcctgtcc gcactgttct gtctcttctg acagcctcca tccaggaagg
                                                                     300
ctctagacta tctgggcatt ttcaaacact gccgcatcaa actgatacaa ctttccacaa
360
cggcatattt tgaatcaaac aaactcttct tgtaatgtcc gctttccgga cagttcccat
                                                                      420
                                                                      480
cccacagtca ggcggccatg aatttgtttg gaggcaacgc tttccaagga ggctgagtcc
                                                                      540
ategecegat ggtgtggetg gteeggeegg ggeaeagtge agageteeta eeegggaete
                                                                      600
tototgacao otagtgtggg agocaggoao actgoacaga cagacacatg gotgaggtat
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gaccetecta gecaaccaaa aggeaageag aggegeacag gatgeaagea egagaagage
                                                                      673
aacttgtcct cga
<210> 74
<211> 583
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 <223> n equals a,t,g, or c
 <400> 74
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                                                                      120
                                                                      180
 cccqggctgc aggaattcgg cacqagacag gtgcatgcac acgccactgt gtgtgtgtat
                                                                      240
 gtgtgtgtgt gtgtgtgt gtaggggaat cttagtctaa agcatcccac tgcaaactaa
                                                                      300
 aagctcttta aagtatatta atgtcacaaa aagttaaggc atttttccat tcttgttagc
                                                                      360
 atgtttcttt taccattttt ctcatttcaa attactttga ctttaaacgt tccctgaaac
                                                                      420
 ttaaatatac tgaggttotg ggaagagota acatgocaac atttotattt tgatacacat
                                                                      480
 atctttctgg caagetgctg agtacctcca gttaagaagc acaggectaa actctcagtg
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540
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                                                                        583
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<210> 75
<211> 801
<212> DNA
<213> Homo sapiens
<400> 75
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                                                                        120
cotggtotga tittititt aaatgoaaat cagactatgt cactottitig citgaagote
                                                                        180
ctcagtggct gcctatggct gtcagggtca gagcctcacc acggcctggg tttcctcctg
                                                                        240
tygeceetgg etttegeete etgetetatt ettateetga aetaegeeaa geeetttete
                                                                        300
aaccccgccc ettgeteect etgtetggaa etacetteec aggeettitt gtgeegttea
                                                                        3 (-0)
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                                                                        480
                                                                        540
ggeeteatgg caeaggeeca teggggteae tgetgtgtte agggeteagt aaggatgeet
                                                                        600
eggtgegett ggatgtggeg etggeegget ggetgggggt geeacetgge gtgatttgtt
gtcacttgct cacttgtcct agatgctgtt tataaaagta ctaatagaac caggcacggt
                                                                        660
ggtttatgcc tgtaatccca gcattttgga agcccaaggt aggcgaatcc cttgagccca
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                                                                        780
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aaaaaaaaa aaaaaactcg a
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 aragggetta ttattggtgt tateacttea tgteteceag agaggeetet gtgggteact
                                                                         180
 geoeccetea atgagttetg aagagagaaa acagaggeeq tggteeagte agtatgggga
                                                                         240
 geactgtgtt ecegacacee cactgegtgt taaggteagg egecacatet tgtagteagt
 tgetttgeeg agtggeteea gettteteta geteetetet gggeeteagt tteeetgeet
                                                                         3130
                                                                         360
 getggecaae agagggeeet gecaaetetg getgeetatg aecagggtgg etceagaggg
                                                                         420
 tgctgctggg aggggtgcca accctamete tetgcaagtg aaactgggca tgccamtcac
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 ctctctgggg cctcagtttc ctcttctgag cattgaggaa atttgggggt ttccatgttc
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 cttccagtca gaaaccagat gctgccatgt cccccaaccc aaggcctcag gaacagtgct
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 ggatggtcat tttngaggtt ttctgtctct gtctctccga ktgaggtttg cttggaaagc
                                                                         660
 taagaataga atccnagcma ggctgtaktg gcggccagct ggaacctgat ataktcacat
                                                                         720
 atgagaactg gtaggcctgc atgccgaccc tctatggacc agaatgggac agaggccaga
                                                                         780
 atatggccat getetteate eteacteetg ecceactgee eteageecag tecteetgtt
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| ccatetgaet gaaaateagg g<br>etgetgtgge etetgagete t<br>geagaaaeee taccetggaa t<br>agcaaettge eatecetete g  | iggagtcaaa<br>iggggagctg   | tggggactgt   | ggaagaggct  | gcccagageg   | 840<br>900<br>960<br>982  |
|---|--|--|---|--|---|
| <210> 77<br><211> 1001<br><212> DNA<br><213> Homo sapiens   |  |  |   |  |   |
| quattoggea egagtactot aaatttette tgeaagacat tggggeagag acaaaaatge acaaagttee ecatateact etteccacgt etttetteccacgt etttetteccacgt etttetteccacgt etttetteccacgt etttettattt eceagttee aagttgette gaacttaca eagagetag gaagteact etttetata egagagetag eactacatggt eactetggtt eaceetteat aatgggagea eagaagaag eaatggagea eaatatgtet agagtggeat gaegtgetaa | cctaaaacat tgctagtctc tcatctccat tggtcaaaat ttttctgagc cacatttttg tcmcttttcm gcmattcact aggcaagaag gaaaatgccc gaacagcatg atgtggagat ccatagcact gattctaaaa ggctgcagat | ctctctcaag tttgttaagc ctgagatcac cattcaacaa cctccaaact agtatyttat cattactatg cacwtctctg aagcagacac agatgcttat agggaaacta tatgaatatt gccttaaggt atagcaagag gtttcagtgg | atagcaagaa<br>ctcagcctgg<br>gtcactaaga<br>gttccaacct<br>agcgsacccc<br>aagaaatmcc<br>cactaccagg<br>cttcttcaca<br>aaaatcatca<br>ccccatgat<br>accatttgag<br>atctaataat<br>aaaagaaaca<br>aaactttatt | ttacctttat actttattgt agttccaaac ctgcctatta accetctgca cagcctgggt gagatctcag gggtggcagg twtctcatga ccaattgcct agagattttg caaactccca aattacatgc | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600<br>660<br>720<br>780<br>840<br>900<br>960<br>1001 |
| <210> 78 <211> 748 <211> 748 <212> DNA <213> Homo sapiens  <400> 78 tcgagggctg ggcctaactg tgcttccttt ctcctggctt gagagctgaa aggaactctc tccaaataga agtttgaaaa ggttccagct tgggttgacg caagggccag aagcagggcc cctcagcatg gtgtgaggct ttcccatcca tggatgtcct actgagaaaa aaaagaggca   | ggtgggcate<br>ctaaagaact<br>ggcaccccct<br>ggcgtgccae<br>tgtgggaagt<br>cttatggage   | cagaatttot cacatatatt agaggaacat cagatcagt ttctaggct cttctaggta  | t ttgacccctgi<br>t ttttaaatto<br>t gcacttctgi<br>t tgaaaccto<br>t ctgctcato<br>t aggatatga<br>c accgggaac   | taattetttt actggeeca cacattgaat cagaactgtee acaaaaagee acaaaaagee aatgaaggtg   | 60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540  |
| actgagaaaa aaaagaggda<br>cttactttgt gcttatagct<br>gcctcattac ccatacagct<br>tttcccaccc cgacactato<br>aacatagaga ctacactcgt   | : gtatgatct<br>: aaagcttaa<br>: agcgacatt  | t tittccica<br>i attaactaa   | t ctctaatge<br>a tcagtggtg  | a attectitee   | 600<br>660<br>720<br>748  |

<210> 79 <211> 586 <212> DNA

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<213> Homo sapiens
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                                                                    120
                                                                    180
aggicatace atgreaceta atatgetgga ecetgeegee teagggaeet teagagetet
                                                                    240
cettttgetg agteateett ttettgaetg gleactitea gaeeeceact gtgaaagest
                                                                    300
gaaccaaaaa taatttctcc tggcctagag gtggtgaatg agagaagagg tttttgtttt
teettgaage cacaaaaagg agttaataag gattgttaga geeateagte tggeattaaa
                                                                    360
gagcagattq gtgtggaatt gggcaccaac aagaatgagt aatatettaa ttaggtttaa
                                                                    420
aaacgatggt accttgcgca tacatatgta agattcctta gagggaagag aggccattcc
                                                                    480
ctgtttgtgt aagagtatat tccttaatta acaaattaag cagcaataga taaaaaaata
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586
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ctactgatgg ataattaaat tatagtatat aaatacaatg gggccgggtg cagtggctca
                                                                    120
geettecaaa gtgetgggat tacaggeatg agecacaaca tecageeeet titetetitt
                                                                    180
cttaccette tttectattt tettttecat tttetttece tecettette tttettteet
                                                                    240
aactattaag gagtagattg aattcaaggt ctttatgtgt gtcagttttt gttttccaac
                                                                    300
                                                                    360
aaatatttot taaaaaccaa ccattgaaac gtaatggtaa ccactggccc ctgtctccac
                                                                    420
ctccacacct aagaagcccc aaatccagat gtgtccatta aaatcagtcc agatcttctt
                                                                    480
taccaagcca ctagatgtca tattaatttc acagcagaat agggaagccc atgccggagc
                                                                    540
546
gcggcc
<210> 81
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<212> DNA
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 atatcaaaag cacaaaaacg tttattctga aaaccaggaa gattgtgatg ttacagaaga
                                                                     120
 agattcaata attccagtcc atttctaggg tactaagtgt ctgatcacct cagygaaaac
                                                                     180
                                                                     240
 aagatacaaa tgaggccaag gtcacaggtc tggccaccct gagtcccttc gcactatttg
                                                                     300
 gtttctcaag ttgagacacg tattcccagt cccagttagc caccttccaa gtgtttgcta
 ctagccttaa tgggtactta gccaaagact acacccaaat ataaccaaag cttatgttaa
                                                                     360
                                                                     4.20
 gtcataagat taatoottoa ataataagga tagoataatt ggotttgtta ootaattota
 cataaacaaa atcatcaaat atcctggcat aactgaaatg acttacagag gaagtagtaa
                                                                     480
                                                                     540
 agettggaag tattetatgg taactgaget gaaaaagggg aaatgecaaa tgttgtaaat
                                                                     600
 gccatcatta ccaataagag tcaccaaatt ctcagaaata ggtaattggc agctcaaggc
 agttagcact acaagattto tottgoottt aaaaaaaaat catttttaag actcottttt
                                                                     660
                                                                     708
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<210> 82 <211> 824

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                                                                       120
truatitita tittigitoo ottagigada tigoaggaat gotgotgaaa totadaggaa
                                                                       180
gttttttaga atttggctta caggagagct gtgctgaatt ttggactagt gcggatgaca
                                                                        240
geagtgette egaegaaate aggttggagt tgtgetteet tteecettee acttettate
                                                                       300
                                                                        360
togtagttto ottootoatg gtgagatoot agaaggagoo ttgttoaaao caaattgtgt
tgjcctggaa gaatttgggc agtagatgta aagggattta tttataactg ccttgtcttt
                                                                        420
                                                                        480
teatgtgatt tettagttat ggttttatgt gaaattttet ttgaagggga aettagaatt
                                                                        540
tatttagtgt gataaaaata gtgccaactg getgggegeg gtygetcaeg cetgtaatee
cagtactitg ggaggccgag gtgggtgaat caccaggtca ggagttcaag accagcctgg
                                                                        600
ccaagatggt gaaacctcgt ctctactaaa aatacaaaaa aaacagctgg gcgtggtggc
                                                                        650
acgcacccgt gatcccagct atteaggagg ctgaggcaga aaatttettg aacccaggag
                                                                        720
                                                                        780
gcagaggttg cagtgagcca agateatgcc actgcactcc agectgggtg acagagcaag
                                                                        824
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                                                                        120
                                                                        180
agactggata ggagtggtat ttatcccaga cggtagcttt gaatttggat ggagataatg
                                                                        240
tatgtaaagg cctctgcagt cacggtctcc agagatgagg ctcttactcc ctgtcttcca
gatecteact ggaatgcace etttgcaaga caceteetee ageecagetg tteetttett
                                                                        300
                                                                        360
gaattcccat agcacttcac tggtatttct ttctagcact taacagttat gtgcctgaca
                                                                        420
tgatggttaa aattttacct teeetttgag aetetgagea eetetagget agggaaggge
                                                                        480
ttggtgcact ccgtgtcctc tatacttgtg ggtaccaaac cgagaagagg atcaatatca
                                                                        540
cttgaggagc tttgaaaaat agattccttt gggaggccga ggtgggccaa tcacagggtc
                                                                        600
aggagattga gaccatcctg gctaatgcag tgaagccccg tctctactaa aaatacaaag
gattggctgg ccttggtggc gggcacctgt ggtcccagct acttgggagg ctgaggcagg
                                                                        660
                                                                        720
agagtggcgt gaacctggga ggcggagctt gcagtgagcc gggattgcgc cgctgtactc
                                                                        780
cagcotgggo aacagagoga gactocatot caaaaaaaaa aaaaaaaaat cgaggggggt
                                                                        789
cccqtaccn
<210> 84
 <211> 811
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                                                                         60
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                                                                         120
 attictcacc gacagicite ccatggical tecatecete etectgeete etecaggeag
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| ageetetetg getgageeea etettagate tgtgaaaggg eageetetea eeetgteaca  | 180  |
|--|------|
| gcacatggaa qaccttqctg tgagcagaqa gaactgctcc cactataggg tccagctttg  | 24'  |
| gcacatggaa qaccttqctg tgagtagga guttaggctg atggctcff cctqctccaq    | 300  |
| toctocaged detgenentt dagetedadg cettadeetg atggetettt cetgetedag  | 350  |
| cotcocctga gotgoccott toatoctato tgoccoctca actaatgoag cacagtotea  | 420  |
| gtaaggtgat ctgtaactct ggctcagggg cttctcaggg ggactgaaga gtaacatcac  | 480  |
| atoccatgaa occaeteagg gaggggggg getggteate actgagteet caettgaaag   | 540  |
| aaagetgaae ttaggeeggt tgtgetggge aeggtggete aegeetataa Leecaacaet  |      |
| ttgggaggee gaggeaggtg ggteacetga ggteaggaat tegagaeeag cetggeeaae  | 500  |
| atggtgaaac taaaaataca aaaaaattag cegageatgg tggcaggeac etgtgateee  | 660  |
| agetacteag gagaateget tgaaccegga aggtggaggt tgeagtaage egagateaca  | 720  |
| ccactgcact ccagectggg cgacagageg agactecate tcaaaaaaaaa aaaaaaaaaa | 780  |
| ctcgaggggg ggcccgtacc caatcgccta t                                 | 811  |
| Cccgaggggg ggood can j   |      |
|  |      |
|  |      |
| <210> 85   |      |
| <211> 1070   |      |
| <212> DNA  |      |
| <213> Homo sapiens   |      |
|  |      |
| <400> 85   |      |
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| tcatccacca gaggccacct gtattcccta tcccacaacc ctagcccctt cctctatctt  | 120  |
| tgaagtggac tatttcatce cetgttteta teatgacagt geettetete atattgacee  | 180  |
| tottgootta taagattoot tgtgattaca otgggtocac otgcataato aaggotaato  | 240  |
| totocatoty gagatottaa tataatoaca totacaaagt coottiggoo attgaagtaa  | 300  |
| catatttata tgtattcatt attaggatgt gggacacttt tgtcagggac agggattttt  | 360  |
| catatttata tgtattcatt attaggatgt gggaddett agoddggggg              | 420  |
| cagectacet tittetteac ettitgecae caeteteage etgiggtete aatgeeagee  | 480  |
| tttacactgc tacccccatt gtctgggtag ktcataccag ycctcaagac tagcctcagg  | 540  |
| cattgeetet tetgggaata cateetetta caggecagga tatgaeteat gggtgeatte  | 600  |
| ctaatagcac ttcamttatt tctactgtca ccacactgat ctgtaattac ttgatttgtc  | 660  |
| tgactcttct gggggcttgt aagcattctg gcacagagaa ctatgactta ctggggctta  | 720  |
| catctcttgc taaacacagt acctaaaatt tagtaggcat tccctcataa acatgaatga  | 780  |
| atgaatcaaa gaatgaataa acatttagga aatgatgttg tgttggtcaa cttctttcct  |      |
| catcactott aaaqataaaa gaatoccaao ccagottott cagacagaao caagcaccac  | 840  |
| atcoctgaga gagcagcaca totgggcago catgtgtgag aagtoggttg cattocccat  | 900  |
| acacagttgt cittgcaget giacicttaa ccactgiaac cacagaagig gggaaacdal  | 960  |
| agggtggggt gaagtgaaaa gaaaattttc caaaacttca tttatctaat aaatacagat  | 1020 |
| atttaaaaaa aaaaaaaaa aactcgaggg ggggcccgta cccaatcgcc              | 1070 |
| accedadada damaran 5 555 555                                       |      |
|  |      |
| <210> 86   |      |
|  |      |
| <211> 727  |      |
| <212> DNA  |      |
| <213> Homo sapiens   |      |
|  |      |
| <400> 86   | 60   |
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| tggaatgcat actggaaaca gctctcattc ctacctttaa agggctcttg gaaagcagtg  | 180  |
| tgacaaccaa ggtcactaaa tggtgagatc atcaagccat tttaagttct ttctcatgtt  | _    |
| attraccage accetgeagg acgttgggea cacateacat cecteagete agecatedag  | 240  |
| cogretagt gatteaceae teattigett aattaataga eaggittigat eacttigtae  | 300  |
| atggaaggca ctgtgccagt gaacaagcag ttggacccag ccctccagta gggaatggac  | 360  |
| agetgaaaat eeatgageaa gaaagaagga aaaagaaaga gttetgagea geeaaaceat  | 420  |
| ttotogatga tttoagagoo ttoattotga goatcagtta tatgetetee agtgtaatga  | 480  |
| ctttatagcc aagcacagta attgatatta ctgtgaaggc ccttaactta tcaagaaatg  | 540  |
| Coccacagoo aagomeng mongaren oo oo oo                              |      |

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600
gttgaggccg ggcacattgg ctcatgccta taatcccagc acgtgggagg ccgaggcagg
                                                                        660
cagatcaett aageceagga gitcaageee ageetgggea acatgatgaa ageeeatete
                                                                        720
tacaaaaaaa aaaaaaaaa actogagggg gggcccggta cccaattcgc cctatagtga
                                                                        727
gtcgtat
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                                                                         60
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aaggggactt ctttgggatg tactctggac ttgttgatag attaagtgta ggtggggtga
                                                                        180
ggaagagaac tcaaagatga caccaggtgt tggagctgag ccacggggag aagggtgcaa
                                                                        240
agggaaagca gtgcgggggc tgggagggga gagggtcagt cctgttttgc ttgtgctgca
                                                                        3:)(:
totgaggage eceteacetg tggaaggaga geagteecag aggeagtggg gtgtgeagtt
                                                                        360
                                                                        420
ctggaactta gaagaatgat cagggggctg ggtgcagtgg ctcacgcctg taatcccagc
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catggtgaaa ccccgtctct actaaaaata taaaaaatta gcagcgcatg gtggcaggca
cctgtagtcc cagctattca ggaggctgag gcaggagagt ggcgtgaacc cgggagacgg
                                                                        600
                                                                        660
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                                                                        690
gtctcaaaaa aaaaaaaaaa aaaaactcga
<210> 88
<211> 896
<212> DNA
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 <400> 88
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                                                                         120
                                                                         180
 gccaattaag caccagattt tgctcttaaa cttttttgga agctgagtag aaattatcct
                                                                         240
 trtgttccat atgatgactt attaaataaa atactttgca caatatgtgc trttagatgg
                                                                         300
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 ttaggtttca gctttgctgt gggtgaaggg aagtgggggg ncttctgttt gttggtgcca
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 ggcattatgc tacatattat acatelytta teteatttga ttyccccaaa teettaagaa
                                                                         540
 gttgaattat tatactcatt ttggaaataa gaaatgaagc ttagagaggg gaagaacagg
                                                                         600
 tttaaateet ggetgtaage eetttggget ttggttttee taaetaggga agaggaataa
                                                                         660
 tagtgatgaa aataacaato atotgatgat otttgtaatt ttactgacgg agtagaagco
                                                                         720
 atcagaagag aatgeeeaca tetteeettt gatagageat etgaettgea teteettagt
                                                                         780
 aactactttc cctcccattc taaactgttc ttttctaggg gccaacctct cctcttgtga
                                                                         840
 acgagetete atcettteet ggatacaeag ettettett cetgeataet tttttetttg
                                                                         896
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<211> 857
<212> DNA
<213> Homo sapiens
<220>
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<223> n equals a,t,g, or c
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                                                                      €0
                                                                      120
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                                                                      180
tttctgtcat tttgaaagtg ttgtatattg atgcccctgg tcatttagga atgcccattt
ctetttgtte tagtgetgtt gtgtgggtga aggttgaeet agtkteagag aaggggtgag
                                                                      240
gaaaggcagg ggcmaaaaga ataaaggaaa gagttycttt tgagtacmaa taaaaactac
                                                                      300
                                                                      360
cayggaaatc tgatttacca aaatgttcta gggattagat tgcaacyatt aaatatgatt
taacygaagg accecteegg cettetetat tecettetet tetactaaaa teettetateg
                                                                      420
aattgcagaa tootttttoa ttkgtotoag taagtaaact toaataaatt ataggtaaaa
                                                                      480
                                                                      540
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gggtgcagtn gctcacgcct gtgaccccag cactttggga ggctgaggcg ggcacatcac
                                                                      600
ctgaggtcag gagttcggga ccagcctggc cgacgtggtg gaaccccgtc tctactagaa
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atacaaaagt tggccaggca tggtggcagg cccggctact tggtaggctg aggcaggaga
                                                                      720
                                                                      780
ategettgag ccagggaggt ggaggttgea gtgageegag ategtgeeae ageegagate
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                                                                      857
aaaaaaaaa aactcga
<210> 90
<211> 561
<212> DNA
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<400> 90
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                                                                      120
atatttgtgt gcatttgcat gtgcaacagt acacacaaac atacataaag agagcaattg
                                                                      180
 ataaggcaaa taaggtaaca tttaacaata atctgataca cataaataga gaaagagcaa
                                                                      240
 ttgataaagt aaatgaggta aaatttaaca ataatctgag caaaaggtat atgtgttttc
                                                                      300
 tttgagacag tctgattctt gcaacttatt ctgtaagttg gaacttattt ccaaacatga
                                                                      360
 ttgaaaaaaa acceegeact tggcaactte ttetettttt cageetagaa atgtetgtgt
 taagtggttt tttatttatt gttgttgttt gttgttattg ttgttttgtt gccaggctcc
                                                                      420
 aactcacaaa atacgagttt aaaaactgcg ttgttatttt tagagatttg tgataataca
                                                                      480
                                                                      540
 561
 aaaaaaaaa aaaaaactcg a
 <210> 91
 <211> 655
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 <400> 91
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 agagagaaat gtttatggtc cttgccttac cctaaattac tgtgcaacct tttggcaagt
                                                                       120
 cactteetet etattetgag titetttate tatteaattg ggttettaga titggtggte
                                                                       180
 totaacacto toccagitti toaattigat gitacattoi acccagigac caaattoata
                                                                       240
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ttocagaago atagtatgot atgtoataco goaaatottg taaacgttoo tgatatggtt
tggctgtgtc cccacccaaa tctcatcttg aattgcagtt cccataatcc acacatgtaa
                                                                     360
caqgagggac caggtggagc taattgaacc atgggggcga teteceecca cetgttettg
                                                                     420
                                                                     480
tgatagtgag ttagttetea tgagatetga tggttttata agggtettte ecetteaetg
ggeacteatt ettetgeete ergrigeeae algaggaagg acalgittige tieceettet
                                                                     540
gocatqattq taagtttoot gaggootooc agotatgoty aactgagagt caattaaact
                                                                     600
                                                                     655
tttttccttt ataaatttaa aaaaaaaaaa aaaaaactct yacggggggg ccctg
<210> 92
<211> 848
<212> DNA
<113> Homo sapiens
<220>
<221> SITE
< 22.2 > (2)
<223> n equals a,t,g, or c
<020>
<221> SITE
<222> (17)
<223> n equals a,t,g, or c
<220>
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<222> (81)
<223> n equals a,t,g, or c
<400> 92
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                                                                     120
ggtctttggc cctagagaaa ctttttatat gagaagtgtt ctctatatac atgtttgagg
                                                                     180
tgactctgga atggattatg aggtcatatc tcaaaatgtc agaaaacgtt atagagcact
                                                                      240
cgaacttttg tatttgctgc ttaacctcaa tattacagcc acaaacaagg ggtaccaaga
                                                                     300
caaagtataa ctgagcataa gcagaaaatg ttaaccctcc aggtttcttt cttaagcaca
                                                                      360
ataaaagtgg gagcgaacaa cacaaggata tttttacatt tgacccgtct caaaagtagc
                                                                      420
                                                                      480-
acaccctatc cttgtgccat tatttgtaca aggaaatata tgattagaag gawtagaacc
                                                                      540
cccagttgtc atcagctttt ttagacacca caggttgtag cagtttgaac aaactgaaaa
                                                                      600
ctttatactt ctgtgtgagc tgaactcaag tttcagaata atcatcgcca tgtgggaggc
                                                                      €60
tttttgttaa atgcagaaga aatttcaaaa tattgtattt atatctgcct tccactgctg
                                                                      720
ccaatttagt aagcatctcc tatacaatcg acaataaaca gcaaatgatg cagttcatag
                                                                      780
agtattttgc acttggggaa aaatatgtat ctgaattgta aaaagaaatg tttggatttt
                                                                      840
848
aaactcga
<210> 93
<211> 612
<212> DNA
<213> Homo sapiens
<400> 93
                                                                       60
gaatteggea egagagegtg ttatteteet geeteeagat eatttagget ttggtaaaae
                                                                      120
ctcggccaat ttggctataa taaaatagat ttccttgagg gcaggattgg ttagggggaa
```

```
180
cagadagete tgggtattat ttcaaaatga tttattttet eeteetettg eetgaageae
                                                                     240
aaggagagtt eteategatt ticaeagtga gaaeetggta ggtaataete atitaageat
gggatectyt yttegtecag accettggag tittaaaatte teagggiggi teaacetgag
                                                                     300
traatttgto aartatggtt taaagtgtto otatggatgt tggotttago tgcaggotoo
                                                                     360
tgtatccacc teceteteta gtttttgaga tggeagtttg titeatgacc tetatgaaga
                                                                     420
480
                                                                     540
ctacctatct atgagaggag tetteettga geecaggagt teaaggitge agtgagecat
                                                                     600
gateatgeca etacaeteca eceteageaa eagagaaaga eastatetem aaaaaaaaaa
                                                                     612
aaaaaaactc ga
<210> 94
<211> 951
<212> DNA
<2213> Homo sapiens
<2200>
<021> SITE
<222> (826)
<223> n equals a,t,g, or c
<400> 94
                                                                        60
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                                                                       120
 ggcgcggagc ccccggagcc cccaaaccgc agacacatcc ccgcgcccca gagccccggc
                                                                       180
 ctgcgcgccc agccgggccc gcgcgatgcc ctcagaccgg cctttcaagc agcggcggag
                                                                       240
 yttcgccgac cgctgtaagg aggtacagca gatccgcgac cagcacccca gcaaaatccc
                                                                       300
 ggtgatcatc gagcgctaca agggtgagaa gcagctgccc gtcctggaca agaccaagtt
                                                                       360
 tttggtcccg gaccatgtca acatgagcga gttggtcaag atcatecggc geegeetgca
                                                                       420
 getgaacece acgeaggeet tetteetget ggtgaaceag cacageatgg tgagtgtgte
                                                                       480
 cacgcccatc geggacatet aegageagga gaaagaegag gaeggettee tetatatggt
                                                                       540
 ctacgcctcc caggaaacct tcggcttctg agccagcagt aggggggctc ggcctgggag
                                                                       600
 teggggggee eeggteagge eetgeecaga gageteetgg tteetgaact gagetgeete
 taccgtggtg ggctgggcag gcatgtgccc ccctagtcag agggcaccaa cccacctayt
                                                                       660
                                                                       720
 ctgcccctgg gtggatcctg ggccggtcgt gttagggttg tccctctggg tgctggctgg
  tgggatgggg gagggtgggg agcagetece ageaeceetg etgtgtggtt catettttt
                                                                       780
                                                                       840
  ttaggecect geetgtetge ceatetgece eteacecace egaggntetg eccaeegect
                                                                       900
  ggacctgccc acccctgaaa gactggcccc tggctccccg cccctcggtc tccacgtggt
                                                                       951
  gtatggatct gtggtcattg tecetetgea gaataaagat tgeteaggee t
 <210> 95
 <211> 2264
 <2112> DNA
 <213> Homo sapiens
 <220>
 <201> SITE
 <222> (299)
 <223> n equals a,t,g, or c
 <220>
 <221> SITE
 <222> (2257)
 <223> n equals a,t,g, or c
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<220>
<2221> SITE
<222> (2264)
<223> n equals a,t,g, or c
<100> 95
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                                                                       120
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 tggttttttt aacaatggto occtacgaac tgcaggagat tettggcacc agscotcect
                                                                       180
 gtteegecar gattetktgg actetqgwgt etetaaggga geatatgetg gaateacagg
                                                                       240
 gaacccatct ggttggcata gctcttcccg agqtcatqat ggcatgagcc aacgtakgna
                                                                       300
                                                                       360
 ggtggcacag ggaaccatcg ccattggaat ggcagettee acteeeggaa agggtgtget
                                                                       420
 tttcaggaaa agccacctat ggagattagg gaagaaaaga aagaagacaa ggtggaaaag
 trgcagtttg aagaggagga ctttccttcc ttgaatccag aagctggcaa acagcatcag
                                                                       480
                                                                       540
 ccatgcagac ctattgggac accttctgga gtatgggaaa acccgcctag tgccaagcaa
 occtocaaga tgctagttat caaaaaagtt tccaaagagg atcctgctgc tgccttctct
                                                                       600
 gotgeattea coteaceagg ateteaceat geaaatggga acaaattgte ateegtggtt
                                                                       660
 ccaagtgtct ataagaacct ggttcctaag cctgtaccac ctccttccaa gcctaatgca
                                                                       720
 tggaaagcta acaggatgga gcacaagtca ggatcccttt cctctagccg ggagtctgct
                                                                       780
                                                                       840
 tttaccagtc caatctctgt taccaaacca gtggtactgg ctagtggtgc agctctgagt
                                                                       900
 teteccaaag agagteeete cageaceaee eetecaattg agateagete etetegtetg
                                                                       960
 accaagttga cccgccgaac caccgacagg aagagtgagt tcctgaaaac tctgaaggat
                                                                      1020
 gaccggaatg gagacttctc agagaataga gactgtgaca agctggaaga tttggaggac
                                                                      1080
 aacagcacac ctgaaccaaa ggaaaatggg gaggaaggct gtcatcaaaa tggtcttgcc
 ctecetgtag tggaagaagg ggaggttete teacactete tagaagcaga geacaggtta
                                                                      1140
 ttgaaagcta tgggttggca ggaatatcct gaaaatgatg agaattgcct tcccctcaca
                                                                      1200
 gaggatgage teaaagagtt ecacatgaag acagageage tgagaagaaa tggetttgga
                                                                      1260
                                                                      1320
 aagaatggct tettgcagag cegeagttee agtetgttet eeeettggag aageaettge
 aaagcagagt ttgaggactc agacaccgaa accagtagca gtgaaacatc agatgacgat
                                                                      1380
                                                                      1440
 geetggaagt aggeatataa atgeteacag ttaaatetga eecagtaaae tetgtgtgtt
 tagggagtat acaaaagaaa togttotttt oottttotta tgttgttgaa tacttoatto
                                                                      1500
 acaagggaaa taatcatatc ccaaagagag agcaattggc ttgttttgct tttgttattg
                                                                      1560
 ttcttccctg ttatctgctt tatagagaga agtttgtgtg gtgggacaga ttttttaaac
                                                                      1620
                                                                      1680
 acactcayac acacacaca atacacaccc agtatatatg gggcgatgca caggtaggag
 ctggcagtgc agggaagagg agacactggt ctgcagcaac agcttctact accagccctt
                                                                      1740
 ggggcactca cccctgtgat caagcaatca ttgtcaatga caaagtgact attgaagtta
                                                                       1800
 taattgtatt aaattaatgc taataatttg gatattttat tttatttttg gctgctcggg
                                                                       1860
                                                                       1920
  taactttagc ccttaaccaa gcatatgtgg gtttttttgg ttgtttttt ttgtttttt
                                                                       1980
  tttctttttc ctttttgggt acagctgtaa aatatttgga tataggaaat gttgtgttat
                                                                       2040
  tettgcagee ttgatattea gggtggattg taaaatataa atttttgtga gattteaaag
                                                                       2100
  attaagatta ttttgataac attatttaca gatttaaaag atgtggttat cacaagtctc
  gagggggaaa ctactgcata aaataactaa cttggaataa atattttgca tcagtttgga
                                                                       2160
                                                                       2220
  2264
  aaaaaaaaa aaaaaaaaaa aaaaaaaagg ggggggnccc cccn
 <210> 96
 <211> 830
 <212> DNA
 <213> Homo sapiens
 <400> 96
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                                                                         60
  gattttactt attgttgata atgctcccac atgtcctctt ttttacgggt gatcttcatt
                                                                        120
  cctaatatca aagtgatatt tcttcctcca ggcaccacct ctttgatcca cacaatggat
                                                                        180
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caaggagtta tagcagcttt taagttctac tacctgagaa gggaggactt ttgcccagtc
                                                                      240
ccatactgca gtggaggaag acactgagaa gactctgatg aaattctgaa cagcatcaag
                                                                      300
aacettgttt aggettggat tatgtegeta aggaetgtag gaatggeace tggaagaaga
                                                                      360
caegeaagag gtttgtcaat aacttcaaag gatttgeeaa ggatgaggaa gttgcaaaaa
                                                                      420
tcaagaaggc tgtggttgag atggcaaaca actttaacct gggtgtggat gtggatgaca
                                                                      480
ttgagtaatt cotagagggg gttcctgagg aattgactaa tgggttgctg ttggaactgg
                                                                      540
aataggagtg catagctgaa gaagaggtaa agaaaaagaa agtgcaggag aagggaaaaa
                                                                      600
agaactccca agaatactca cagtgatggg tttagcagaa gcttcttcag actccaacaa
                                                                      660
geteettaag aagtetgaaa acatggaeee caaaaetgaa aggtttteae taatagagag
                                                                      720
gaaagtteat ggtgeattat etgeetacaa geaaaaceag gatteaaaaa accetttgag
                                                                      780
                                                                      830
(tggagcttc aaagcacaaa aaaaaaaaaa aaaaaaaaa aagggcggcc
<210> 97
<211> 886
<212> DNA
<213> Homo sapiens
<220>
<221> SITE
<222> (92)
<223> n equals a,t,g, or c
<220>
<221> SITE
<222> (886)
<223> n equals a,t,g, or c
<400> 97
 atttcatttt agggcatact gggcttactc tecteccage tgtetgtgga ttgatttgat
                                                                       6.0
 tttaatgttc gagttttaca gcaacagctg anaaaccatg aactattcta ggaactgtgt
                                                                       120
 180
 aageettgga etttggaggg acagaaagee accageeaat ggagaacaaa gagatgttte
                                                                       240
                                                                       300
 cettteettt ettteacett gteattetgg gttteettet getteactet tteetteese
 cttaaaagtg gtatteetgg ttggtetgte tgtetgteet tgteettgtg gtgateetgg
                                                                       360
 catggtgata tgctccactt tgcattatcc atggtctctt accagcgcac aagtcagtgg
                                                                       420
                                                                       480
 ggaggatcta accacgcctg gtggtgagga agctgaattt ccaggcctgc gtcccatgta
 gcctctccat gaactgcaga aggcatgttc tgcatggtta ccagtaagtg gctccctctc
                                                                       540
 acceptettca ttetcaaate agagcaaact ttagetette getecattet acactetaet
                                                                       600
 tgetetgete ecetecetee aaccagggtt catgteagtg cacaceceat gtgeeetgge
                                                                       660
                                                                       720
 gaagetggtg etgtgagtga tgtttcccat acaactcagg gatgccaggt ggettaccet
 gagatagtca ttttgggcac ataacagtgt aggaatgaaa catggatttc attgatattt
                                                                       780
 aaatctgtca atttcatttt ttgttaatgt tttcccctga tgacttttta gcaatttaac
                                                                       840
                                                                       886
 aaataaaatg gacaattgtc ttaaaaaaaa aaaaaaaaa ctcgan
 <210> 98
 <211> 597
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (12)
 <223> n equals a,t,g, or c
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60

120

180

240

300

360

420

480

540

597

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<400 > 98
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cytotagact atgateceeg getgeagaat teggeaegag eagteeagaa aetgegtgee
etaccettig cutgggeeee tetaccagta tgtecageat gtgeeegggg geeeteaget
cceptgggge ccageccaee caagacacag ofottggteg tgaacatgaa gatgayecaa
actotagtgg ctottoctga aagaaatgag aatgoocage cacacccatg cacgottigt
 tetttttttat ttaatactga ggaaceggag tggaggggte etgeeggget geagtgaeee
 tgagggaagt caggagagee etgggetqea qaagagteee eecacagget eegaagcaag
 cttgtcctgg tgcattcaga ctgctcacag caggetttqq gccctcactc tccagatccc
 agagageest ecagggetee cagetetegg greagtgees amgteetega aggggggeeg
 gtaaccaatt egecetatag tgagtegtat tacaatteae tggeegtegt tttacaa
<210> 99
<7:1> 66
<212> PRT
<113> Homo sapiens
<220>
<221> SITE
<222> (66)
<223> Xaa equals stop translation
<400> 99
Met Phe Leu Gly Asn Ser Leu Glu Thr Leu Thr Asn Arg Ile Leu Val
                                      10
Ser Leu Ala Ser Val Phe Leu Leu Pro Pro Arg Lys Gly Ala Gly Leu
                                                      3.0
                                  25
Cys Ser Arg Gln Asp Arg Arg Ala Pro His Ala Tyr Thr Ser Leu Pro
                              40
 Glu Leu Ser Pro Arg Ala Ser Gly Pro Cys Leu Glu Thr Gly Leu Ala
                                              60
                          55
 Leu Xaa
  65
 <210> 100
 <211> 72
 <:212> PPT
 <2213> Homo sapiens
 <220>
 <2221> SITE
 <222> (72)
 <223> Xaa equals stop translation
 <400> 100
 Met Tyr Gln Glu Thr Arg Ser Ser Pro Thr Asn Thr Leu Arg Pro Trp
                                      10
                    5
```

```
Pro Arg Gly Thr Ser Arg Cys Leu Arg Cys Ser Phe Cys Arg Leu Ser 20 25 30
```

Phe Ala His Ser Gln Gly Ile Gln Gln Let Ser Cys Ser Leu Ser Arg 35 40 45

Thr Asp Ser Arg Ser Phe Thr Ile Ser Lys Thr Leu Trp Ala His Asn 50 55 60

Arg Arg His Ser Phe Gln Gly Xaa 65 70

<210> 101

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (51)

<223> Xaa equals stop translation

<400> 101

Met Asn Ala Tyr Arg Val Lys Pro Ala Val Phe Asp Leu Leu Leu Ala 1 5 10 15

Val Gly Ile Ala Ala Tyr Leu Gly Met Ala Tyr Val Ala Val Gln His

Phe Ser Leu Leu Tyr Lys Thr Val Gln Arg Leu Leu Val Lys Ala Lys
35 40 45

Thr Gln Xaa 50

<210> 102

<211> 221

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (221)

<223> Xaa equals stop translation

<400> 102

Met Asn Val Phe Arg Ile Leu Gly Asp Leu Ser His Leu Leu Ala Met

1 5 10 15

Ile Leu Leu Gly Lys Ile Trp Arg Ser Lys Cys Cys Lys Gly Ile
20 25 30

Ser Gly Lys Ser Gln Ile Leu Phe Ala Leu Val Phe Thr Thr Arg Tyr

35 40 45

Leu Asp Leu Phe Thr Asn Phe Ile Ser Ile Tyr Asn Thr Val Met Lys 50 55 60

Val Val Phe Leu Leu Cys Ala Tyr Val Thr Val Tyr Met Ile Tyr Gly
65 70 75 80

Lys Phe Arg Lys Thr Phe Asp Ser Glu Asn Asp Thr Phe Arg Leu Glu 85 90 95

Phe Leu Leu Val Pro Val Ile Gly Leu Ser Phe Leu Glu Asn Tyr Ser 100 105 110

Phe Thr Leu Leu Glu Ile Leu Trp Thr Phe Ser Ile Tyr Leu Glu Ser 115 120 125

Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys Thr Gly Glu Ala 130 135 140

Glu Thr Ile Thr Thr His Tyr Leu Phe Phe Leu Gly Leu Tyr Arg Ala 145 150 155 160

Leu Tyr Leu Ala Asn Trp Ile Arg Arg Tyr Gln Thr Glu Asn Phe Tyr 165 170 175

Asp Gln Ile Ala Val Val Ser Gly Val Val Gln Thr Ile Phe Tyr Cys 180 185 190

Asp Phe Phe Tyr Leu Tyr Gly Thr Lys Gly Arg Ser Trp Asp Asp Ser 195 200 205

Asn Ala Asp Thr Gly Leu Arg Ser Tyr Ser Ser Ile Xaa 210 215 220

<210> 103

<211> 114

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (114)

<223> Xaa equals stop translation

<400> 103

Met Leu Ser His Val Phe Pro Ile Cys Thr Arg Pro Cys Leu Ser Met

Tyr Phe Pro Cys Val Pro Ser Met Tyr Leu Val Tyr Phe Leu Pro Leu 20 25 30

Asn His Gly Ile Leu Leu Thr Glu Pro Tyr Val Pro Tyr Pro Ala His

Cys Tyr Ala Leu Phe Pro Asn Ser Cys Leu Val Gly Pro Ser Thr Pro 50

Ser Pro Cys His Arg Ile Ser Ile Ser Ala Gln Ile Pro Pro Ile Ser

Ile Ala Phe Met Tyr Tyr Pro Gln Ser Thr Leu Thr Ile Ile Phe Ser 85

Gln Asp Cys Ser Leu Leu Phe Cys Val Phe Leu Arg Gly Ile Lys Glu 105

Lys Xaa

<210> 104

<211> 132

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (132)

<223> Xaa equals stop translation

<400> 104

Met Glu Asn Ile Ser Xaa Asp Val Ile Val Gly Arg Cys Leu Ala Ile 10

Leu Lys Gly Ile Phe Gly Ser Ser Ala Val Pro Gln Pro Lys Glu Thr

Val Val Ser Arg Trp Arg Ala Asp Pro Tyr Val Ala Ala Gly Ser Ser 35

Gly Asn Asp Tyr Asp Leu Met Ala Gln Pro Ile Thr Pro Gly Pro Ser

Ile Pro Gly Ala Pro Gln Pro Ile Pro Arg Leu Phe Phe Ala Giy Glu

His Thr Ile Arg Asn Tyr Pro Ala Thr Val His Gly Ala Leu Leu Ser

Gly Leu Arg Glu Ala Gly Arg Ile Ala Asp Gln Phe Leu Gly Ala Met 105

Tyr Thr Leu Pro Arg Gln Ala Thr Pro Gly Val Pro Ala Gln Gln Ser

125 120 115

Pro Ser Met Xaa 130

<210> 105

<111> 88

<1:12> PRT

<113> Homo sapiens

<220>

<221> SITE

<222> (88)

<223> Xaa equals stop translation

<400> 105

Met Glu Asn Thr Phe Phe Val Phe Leu Val Ser Ala Leu Leu Leu Ala 10

Val Ile Tyr Leu Asn Ile Gln Val Val Arg Gly Gln Arg Lys Val Ile 20

Cys Leu Leu Lys Glu Gln Ile Ser Asn Glu Gly Glu Asp Lys Ile Phe

Leu Ile Asn Lys Leu His Ser Ile Tyr Glu Arg Lys Glu Arg Glu Glu

Arg Ser Arg Val Gly Thr Thr Glu Glu Ala Ala Pro Pro Ala Leu 70 65

Leu Thr Asp Glu Gln Asp Ala Xaa 85

<210> 106

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (64)

<223> Xaa equals stop translation

<400> 106

Met Ser Ala Ala Ser Phe Trp Pro Arg Pro Val Ala Ser Ile Ser Val

Phe Ile Leu Leu Gly Ser Ser Val Thr Thr Ser Lys Thr Arg Ser Gly 25 20

Val Ile Ser Ser Ala Gly Lys Pro Ile Trp Val Gln Ser Pro His Leu 35 40

Ala Leu Leu Glu Val Leu Leu Gln Lys Gly Ile Val Pro Glu Lys Xaa 55 σŨ

<210> 107

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (41)

<223> Xaa equals stop translation

<400> 107

Met Leu Ser Leu Thr Val Ser Leu Lys Ser Val Ser Ile Ala Ala Gln 10

Ser Leu Phe Leu Asp Leu His Phe Pro Ile Gln Met Thr Leu Val His 25 20

Lys Glu Ile Ala Lys Leu Glu Thr Xaa 35

<210> 108

<211> 48

<212> PRT

<213> Homo sapiens

<400> 108

Met Thr Leu Tyr Leu Asn Thr Asn Lys Asn Lys Pro Ser Ala Leu Tyr 10 5

Ser Leu Phe Phe Cys Phe Ile Ser Thr Pro Tyr Thr Tyr Gly Leu Gln

Ile Cys Tyr Lys Cys Phe Phe Ile Tyr Ile Phe Val Ile Cys Leu Tyr 45 40 35

<210> 109

<211> 38

<212> PRT

<213> Homo sapiens

<400> 109

Mot Phe Leu Thr Tyr Leu Thr Tyr Asn Val Ile Ser Leu Asn Glu Val

PCT/US98/15949

15 10 Val Ser Thr Ser Ala His Gln Ile Ala Val Tle Val Asn Tyr Leu Phe 25 20 Met Gly Asp Asn Leu Phe 35 <210> 110 <211> 45 <2111> PRT <213> Homo sapiens <220> <221> SITE <2222> (45) <223> Xaa equals stop translation <400> 110 Met Pro His Pro Ile Trp Cys Tyr Arg Asn Ser Ala Arg Lys Val His 5 Leu Phe Ala Cys Leu Phe Ile Leu Tyr Ile Leu Pro Ile Leu Tyr Ser Cys Thr Lys Asp Leu Ile Glu Asn Leu Lys Ser Ser Xaa 40 <210> 111 <211> 39 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (39) <223> Xaa equals stop translation <400> 111 Met Leu Arg Ile Lys Ser Cys Leu Leu Phe Phe Ile Phe Pro 10 15 Phe Asn Ile Lys Asp Ser Gln Val Pro Ala Asn Tyr Ile Ala Thr Phe 25 20 Ser Arg Lys Cys Ser Phe Xaa 35 <210> 112 <211> 25

<212> PRT

<213> Homo sapiens

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<2.20>
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<2333> (25)
<223 - Xaa equals stop translation
<400> 112
Met Ser Leu Gln Pro Pro Phe Val Met Leu Leu Ser Thr Ala Gln
                       10
His His Glu Leu Gly Ala Asp Thr Xaa
            20
<210> 113
<211> 50
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (50)
 <223> Xaa equals stop translation
 Met Pro Lys Gly Ile Leu Val Ser Phe Leu Cys Ala Leu Ser Pro Arg
                                    10
 Thr Gly Met Leu Gly Val Ser Phe Leu Leu Phe Ile Gly Ile Leu Leu
             20 . 25
 Arg His Thr Ser Cys Leu Phe Cys Met Val Phe Ala Lys Met Pro Leu
                            40
 Ala Xaa
      50
 <210> 114
 <211> 54
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
  <222> (54)
  <223> Xaa equals stop translation
  <400> 114
  Met Cys Pro Pro Ser Gln Arg Ala Pro Thr His Leu Leu Cys Pro Trp
                                     10
  Val Asp Pro Gly Pro Val Val Leu Gly Leu Ser Leu Trp Val Leu Ala
                                 25
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Gly Gly Met Gly Glu Gly Glu Gln Leu Pro Ala Pro Leu Leu Cys 40

Gly Ser Ser Phe Phe Xaa

<210> 115

<211> 268

<212> PRT

<213> Homo sapiens

<400> 115

Met Glu Val Ala Glu Pro Ser Ser Pro Thr Glu Glu Glu Glu Glu Glu

Glu Glu His Ser Ala Glu Pro Arg Pro Arg Thr Arg Ser Asn Pro Glu

Gly Ala Glu Asp Arg Ala Val Gly Ala Gln Ala Ser Val Gly Ser Arg

Ser Glu Gly Glu Gly Glu Ala Ala Ser Ala Asp Asp Gly Ser Leu Asn

Thr Ser Gly Ala Gly Pro Lys Ser Trp Gln Val Pro Pro Pro Ala Pro

Glu Val Gln Ile Arg Thr Pro Arg Val Asn Cys Pro Glu Lys Val Ile

Ile Cys Leu Asp Leu Ser Glu Glu Met Ser Leu Pro Lys Leu Glu Ser 100

Phe Asn Gly Ser Lys Thr Asn Ala Leu Asn Val Ser Gln Lys Met Ile 115

Glu Met Phe Val Arg Thr Lys His Lys Ile Asp Lys Ser His Glu Phe 135

Ala Leu Val Val Asn Asp Asp Thr Ala Trp Leu Ser Gly Leu Thr 155 145

Ser Asp Pro Arg Glu Leu Cys Ser Cys Leu Tyr Asp Leu Glu Thr Ala 170

Ser Cys Ser Thr Phe Asn Leu Glu Gly Leu Phe Ser Leu Ile Gln Gln 185

Lys Thr Glu Leu Pro Val Thr Glu Asn Val Gln Thr Ile Pro Pro Pro 200

Tyr Val Val Arg Thr Ile Leu Val Tyr Ser Arg Pro Pro Cys Gln Pro 220 215

Gln Phe Ser Leu Thr Glu Pro Met Lys Lys Met Phe Gln Cys Pro Tyr 225 235 240

Phe Phe Phe Asp Val Val Tyr lle His Asn Gly Thr Glu Glu Lys Glu 245 250 250

Glu Glu Asp Glu Ala Ile Glu Val Glu Ala Thr Val 260 265

<210> 116

<211> 38

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (38)

<223> Xaa equals stop translation

<400> 116

Met Gly Cys Phe Pro Leu Trp Leu Val Thr Leu Ala Val Gly Asp Ala

Leu Pro Pro Thr Ala Cys Glu Leu Trp Gly Val Pro Ala Pro Pro Leu 20 25 30

His Leu Ala Glu Glu Xaa

<210> 117

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (122)

<223> Xaa equals stop translation

<400> 117

Met Gly Leu Trp Leu Gly Met Leu Ala Cys Val Phe Leu Ala Thr Ala 1 5 10 15

Ala Phe Val Ala Tyr Thr Ala Arg Leu Asp Trp Lys Leu Ala Ala Glu 20 25 30

Glu Ala Lys Lys His Ser Gly Arg Gln Gln Gln Gln Arg Ala Glu Ser 35 40 45

Thr Ala Thr Arg Pro Gly Pro Glu Lys Ala Val Leu Ser Ser Val Ala 50 55 60

Thr Gly Ser Ser Pro Gly Ile Thr Leu Thr Thr Tyr Ser Arg Ser Glu

65 70 75 80

Cys His Val Asp Phe Phe Arg Thr Pro Glu Glu Ala His Ala Leu Ser 85 90 95

Ala Pro Thr Ser Arg Leu Ser Val Lys Gin Leu Val Ile Arg Arg Gly
100 105 110

Ala Ala Leu Gly Ala Ala Ser Ala His Xaa 115 120

<210> 118

<211> 34

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (34)

<223> Xaa equals stop translation

<400> 118

Met Ile Gln Thr Phe Pro Ala Tyr Leu Cys Leu Pro Leu Phe Tyr Val 1 5 10 15

Leu Asp Leu Ala Leu Ala Ser Ala Pro Val Leu Ser His Ser Ala Leu 20 25 30

Leu Xaa

<210> 119

<211> 178

<212> PRT

<213> Homo sapiens

<400> 119

Met Gln Asn Asp Phe Gly Gln Val Trp Arg Trp Val Lys Glu Asp Ser

1 5 10 15

Ser Tyr Ala Asn Val Gln Asp Gly Phe Asn Gly Asp Thr Pro Leu Ile 20 25 30

Cys Ala Cys Arg Arg Gly His Val Arg Ile Val Ser Phe Leu Leu Arg 35 40 45

Arg Asn Ala Asn Val Asn Leu Lys Asn Gln Lys Glu Arg Thr Cys Leu 50 60

His Tyr Ala Val Lys Lys Lys Phe Thr Phe Ile Asp Tyr Leu Leu Ile 65 70 75 80

Ile Leu Leu Met Pro Val Leu Leu Ile Gly Tyr Phe Leu Met Val Ser

95 90 85

Lys Thr Lys Gln Asn Glu Ala Leu Val Ard Met Leu Leu Asp Ala Gly 100 105 110

Val Glu Val Asn Ala Thr Asp Cys Tyr Gly Cys Thr Ala Leu His Tyr 120

Ala Cys Glu Met Lys Asn Gln Ser Leu Ile Pro Leu Leu Glu Ala 140 135

Arg Ala Asp Pro Thr Ile Lys Asn Lys His Gly Glu Ser Ser Leu Asp 145 150 155

Ile Ala Arg Arg Leu Lys Phe Ser Gln Ile Glu Leu Met Leu Arg Lys 170 165

Ala Leu

<210> 120

<211> 46

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (46)

<223> Xaa equals stop translation

<400> 120

Met Ile Leu Gln Ser Leu Leu Phe Leu Gln Arg Leu Leu Met Ile Ser 10

Thr Lys Pro Ala Val Val Leu Leu Trp Pro Leu Leu Lys Lys Val Glu 20

Asn Thr Leu Met Gln His Val His Pro Asn Leu Pro Ala Xaa 40

<210> 121

<211> 67

<212> PRT

<213> Homo sapiens

<220>

-:::1> SITE

<202> (12)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (67)

<223> Xaa equals stop translation

<400> 121

Met Asn Leu Ser Ile Ile Leu Pro Asn Ser Phe Xaa His Leu Cys Asn 1 5 10 15

Phe Ser Leu Phe Leu Leu Pro Leu Pro Val Pro Ser Gln Pro Leu Ile 20 25 30

Cys Ser Gly Asn Tyr Gln Ser Ser Phe Cys His Tyr Arg Leu 11e Cys 35 40 45

Ile Phe Lys Glu Ile Tyr Ile His Gly Thr Ile His His Leu Cys Phe 50 55 60

Val Val Xaa

<210> 122

<211> 337

<212> PRT

<213> Homo sapiens

<400> 122

Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu Lys Leu Gln
1 5 10 15

Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu Ala Gly Lys Gln 20 25 30

His Gln Pro Cys Arg Pro Ile Gly Thr Pro Ser Gly Val Trp Glu Asn 35 40 45

Pro Pro Ser Ala Lys Gln Pro Ser Lys Met Leu Val Ile Lys Lys Val 50 60

Ser Lys Glu Asp Pro Ala Ala Ala Phe Ser Ala Ala Phe Thr Ser Pro 65 70 75 80

Gly Ser His His Ala Asn Gly Asn Lys Leu Ser Ser Val Val Pro Ser 85 90 95

Val Tyr Lys Asn Leu Val Pro Lys Pro Val Pro Pro Pro Ser Lys Pro 100 105 110

Asn Ala Trp Lys Ala Asn Arg Met Glu His Lys Ser Gly Ser Leu Ser 115 120 125

Ser Ser Arg Glu Ser Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro 130 135 140

Val Val Leu Ala Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu Ser Pro 145 150 155 160 Ser Ser Thr Thr Pro Pro Ile Glu Ile Ser Ser Ser Arg Leu Thr Lys 170 165

Leu Thr Arg Arg Thr Thr Asp Arg Lys Ser Glu Phe Leu Lys Thr Leu 185 180

Lys Asp Asp Arg Asn Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys 205 200

Leu Glu Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn Gly 215 210

Glu Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro Val Val Glu Glu 235 230

Gly Glu Val Leu Ser His Ser Leu Glu Ala Glu His Arg Leu Leu Lys 250 255 245

Ala Met Gly Trp Gln Glu Tyr Pro Glu Asn Asp Glu Asn Cys Leu Pro 265

Leu Thr Glu Asp Glu Leu Lys Glu Phe His Met Lys Thr Glu Gln Leu 280

Arg Arg Asn Gly Phe Gly Lys Asn Gly Phe Leu Gln Ser Arg Ser Ser 295 290

Ser Leu Phe Ser Pro Trp Arg Ser Thr Cys Lys Ala Glu Phe Glu Asp 315

Ser Asp Thr Glu Thr Ser Ser Ser Glu Thr Ser Asp Asp Ala Trp 330 325

Lys

<210> 123

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (69)

<223> Xaa equals stop translation

<400> 123

Met Lys Glu Ala Leu His Trp Ala Leu Phe Ser Met Gln Ala Thr Gly 10

His Val Leu Leu His Leu Leu Pro Ala Ala Pro Arg Cys His 25

Arg Gly Arg Ala Ser Pro Gln Gly Gln Gly Leu Ile Pro His Pro Asp

45 40 35

Leu Ser Glu Asp Thr Ala Val Lys Ala Gln Ala Leu Ala Phe Pro Ser 60 55

Gla Gly Leu Asp Xaa €5

<210> 124

<211> 77

<112> PRT

<213> Homo sapiens

<220>

<121> SITE

<222> (60)

<223> Xaa equals any of the naturally occurring L-amino acids

<320>

<221> SITE

<222> (77)

<223> Xaa equals stop translation

<400> 124

Met Asn Gly Gln Arg Met Asp Glu Leu Phe Val Leu Ile Arg Asp Gly 1.0

Phe Leu Leu Pro Thr Gly Leu Ser Ser Leu Ala Gln Leu Leu Leu 25

Glu Ile Ile Glu Phe Arg Ala Ala Gly Trp Lys Thr Thr Pro Ala Ala

His Lys Tyr Tyr Tyr Ser Glu Ser Pro Thr Arg Xaa Pro Asp Gln Gly 55

Phe Leu Thr Ser Thr Gly Leu Ser Ser Thr His Leu Xaa 70 65

<210> 125

<211> 22

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (22)

<223> Xaa equals stop translation

<400> 125

Met Leu Leu Phe Leu Ile Leu Phe Phe Tyr Glu Lys Asn Gln Cys Gln 10 5 1

```
Ser Ala Asp Pro Leu Xaa
  20
```

<210> 126

<211> 37

<212> PRT

<213> Homo sapiens

< 2.2.0>

<221> SITE

<222> (37)

<223> Xaa equals stop translation

<400> 126

Met Gly Lys Leu Leu Phe Pro Leu Leu Leu Ala Pro Phe Ser Pro Ile 10

Asn Lys Tyr Ile Leu His Phe Ala Arg Asp Gly Val Glu Glu Val Leu 25 20

Lys Phe Val Ser Xaa 35

<210> 127

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (62)

<223> Xaa equals stop translation

Met Leu Val Val Ala Val Ile Phe Leu His Gly Ala Gly Ala Met Asn 10

Tyr Leu Ile Ala Lys Ile Leu Glu Val Gln Gly Leu Arg Glu Val Pro 25

Cys Thr Tyr Asn Thr Arg Gly Ile Ala Pro Pro Gly Gly Asn Val Gly 40 35

Phe Glu Ala Ala Ser Val Val Asp Arg Pro Cys Gly Gln Xaa 55 50

<210> 128

<211> 46

<212> PRT

<213> Homo sapiens

<220>

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<221> SITE
<222> (41)
<2003> Maa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
< 222 > (46)
<223> Xaa equals stop translation
<400> 128
Met Gly Phe Phe Glu Thr Ile Lys Lcu Leu Trp Val Val Leu Ile
                                     10
Asp Cys Val Gly Val Gly Leu Leu Ile Ala Thr Leu Met Trp Phe Ile
                      25
Ser Asn Lys Tyr Leu Val Lys Arg Xaa Glu Gln Arg Leu Xaa
                            40
 <210> 129
 <211> 56
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (56)
 <223> Xaa equals stop translation
 <400> 129
 Met Cys Ala Leu His Trp Leu His Trp Leu Ala Ser Trp Leu Cys Ser
                                      10
 Gln Pro Cys Leu Leu Pro Ser Ser Pro Val Leu Cys Gln Ala Phe
                                 25
 Ser Pro Ser Pro Val Ser Ser Pro Leu Arg Gln Ala Ile Ala Pro Ile
                              40
          35
  Trp Leu Gly Arg His Arg Gln Xaa
       50
  <210> 130
  <211> 63
  <212> PRT
  <213> Homo sapiens
  <220>
  <221> SITE
  <222> (63)
  <223> Xaa equals stop translation
  <400> 130
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Met Arg Glu Asp Pro Thr Trp Gly Arg Ser Leu Lys Ser Ser Leu Lys 1 5 10

Ile Leu Ser Asp Leu Ser Tyr Ser Leu Val Leu Trp Leu Thr Ala Ile

Leu Gly Leu Thr Ala Gln Lys Ser Gln Glu Lys Ser Gly Arg Ala Arg 40

Ile Cln Ser Ile Cys Ser Tyr Asn Val Ala Thr Ser Phe Ala Xaa 55

<210> 131

<211> 35

<2:12> PRT

<1:13> Homo sapiens

<220>

<221> SITE

<222> (35)

<223> Xaa equals stop translation

<400> 131

Met Leu Ser Leu Met Ser His Leu His Val Gln Gln His Leu Ser Ser 1 5

Ile Leu Leu Ile Leu Ile Val Phe Ala Phe Leu Ser Asn Pro Phe Leu

Asn Gln Xaa

<210> 132

<211> 33

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (33)

<223> Xaa equals stop translation

<400> 132

Met Thr Arg Trp Leu Val Gln His His Thr Ser Leu Val Gln Val Leu

Ala Val Ser Phe Pro Ala Glu Gly Pro Gly Thr Glu Phe Pro Thr Ser 20 25

Xaa

```
<210> 133
<211: 118
<212> PRT
<213 - Homo sapiens
<2000
<221> SITE
<212> (118)
<223> Xaa equals stop translation
<400> 133
Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly Gly Leu Ser Leu
 1 5
Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu Ala Val Leu Ser
Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val Val Leu Val Val
Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr Val Lys Val Ala
     50
Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala Leu Leu Ala Ala
Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala Val Ala Met Phe
                                     90
 Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg Lys Asp Cys Ala
            100
 Asp Pro Cys Asp Ser Xaa
       115
 <210> 134
 <211> 146
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (146)
 <223> Xaa equals stop translation
  <400> 134
 Met Leu Thr Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser
  Pro Pro Trp Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu
                                  25
               20
```

Met Pro Ser Pro Arg Ile Trp Pro Gln Val Thr Pro Thr Gly Arg Ser

Ala Ser Val Arg Ser Glu Gly Asn Thr Ser Ser Leu Trp Asn Phe Ser 55

Ala Gly Gln Asp Val His Ala Ile Val Thr Arg Thr Cys Glu Ser Val 75 70

Leu Ser Ser Ala Val Tyr Thr His Gly Cys Gly Cys Val Arg Ser Ala 85

Thr Asn Ile Thr Cys Gln Ser Ser Gly Gln Gln Arg Gln Ala Ala Arg 105

Glm Glu Glu Glu Asm Ser Ile Cys Lys Ala His Asp Ser Arg Glu Gly 120

Arg Leu Gly Tyr Pro Leu Ser Ala His Gln Pro Gly Ser Gly Gly Pro 140 135

Asn Xaa 145

<210> 135

<211> 45

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (45)

<223> Xaa equals stop translation

Met Asn Arg Ile Leu Ser Tyr Leu Glu Thr Gly Phe Phe Ser Leu Pro 10

Leu Tyr Phe Phe Leu Thr Tyr Glu Leu His Val Pro Leu Met Lys Thr 25 20

Met Asn Trp Thr Cys Thr Thr Val His Val Ile Asp Xaa 40

<210> 136

<211> 134

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (114)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE <222> (134)

<223> Xaa equals stop translation

<400> 136

Mot Ala Lou Mot Glu Val Asn Lou Lou Sor Gly Phe Met Val Pro Ser 10

Glu Ala Ile Ser Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His 25

Gly Lys Leu Asn Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys 40

Val Asn Ile Pro Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp

Ala Ser Val Ser Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val 70

Arg Ser Tyr Asn Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser 90

Asp Val Gln Gly Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His 105 100

His Xaa Ser Ser Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe 120

Met Glu Leu Trp Leu Xaa 130

<210> 137

<211> 26

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (26)

<223> Xaa equals stop translation

<400> 137

Met Gln Lys Arg Glu Arg Lys Leu Tyr Val Ile Phe Leu Tyr Leu Ala

Phe Ile Leu Leu His Trp Gln Ser Gly Xaa

<210> 138

<211> 19

<212> PRT

<213> Homo sapiens

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<220>
<221> SITE
<221> (19)
<233> Xaa equals stop translation
<400> 138
Ile Pro Asn Glu Met Ala Gly Ser Ile Trp Pro Leu Gly Tyr Leu Ala
                5
Thr Leu Xaa
<110> 139
<211> 93
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (93)
<223> Xaa equals stop translation
<4(10> 139
Met Leu Arg Cys Ala Trp Ala Leu Ala Pro Pro Val Pro Pro Pro Leu
Val Thr Asp Leu Pro Phe Phe Phe Thr Leu Ser Pro Phe Leu Phe Ala
 Leu Glu Pro Pro Leu Pro Asp Leu Thr Asp Ser Ala Ser Met Ser Val
                             40
 Ile Val Asp Arg Arg Ser Arg Gly Ser Asp Thr Asn Cys Trp Leu Leu
```

Ile Val Asp Arg Arg Ser Arg Gly Ser Asp Int Ash Cys 11p 250 250 50 55 60

Asn Arg Arg Ser Lys His Pro Gly Ala Pro Arg Met Cys Thr Cys Lys 65 70 75 80

Ala Asn Ser Asn Lys Tyr Thr Ser Ser Leu Thr Asp Xaa 85 90

<210> 140 <211> 40 <112> PRT <213> Homo sapiens

<400> 140
Met Arg Ala Asn Phe Arg Cys Trp Leu His Cys Thr Leu Tyr Leu Leu
1 5 10 15

Cys Ser Pro Pro Ser Asn Gln Gly Ser Cys Gln Cys Thr Pro His Val 20 25 30 Pro Trp Arg Ser Trp Cys Cys Glu 35 40

<210> 141

<211> 82

<212> PRT

<213> Homo sapiens

<400> 141

Met Ser Ala His Cys Asn Leu His Leu Pro Gly Ser Ser Asn Ser Pro 1 5 10 15

Thr Ser Ala Ser Gln Val Ala Gly Ile Thr Arg Glu Glu Ala Glu Gly 20 25 30

Gln Gly Gly Lys Gly Ile Gly Ser Gln Val His Gly Pro Leu Val Lys

Pro Pro Leu Leu Trp Gly Leu Arg Lys His Arg Gly Gly Val Ser Cys 50 55 60

Ser Ala Cys Pro His Ser Pro Ala Asn Asn Val Val Thr Ser Val Pro 65 70 75 80

Asn Leu

<210> 142

<211> 76

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (76)

<223> Xaa equals stop translation

<400> 142

Met Asn Met Cys Trp Gln Ile Pro Asn Phe Ile Leu Ile Gln Val Ser

1 5 10 15

Ser Glu Tyr Val His Ile Leu Ile Val Ile Val Thr Lys Thr Pro Gly 20 25 30

Val Gln Ser Gly Ser Cys Cys Ser Leu His Arg Lys Pro Met Pro Glu 35 40 45

Thr Thr Ser Val Ala Lys Glu Glu Gly Leu Ile Gly Cys Cys Ser Arg
50 55 60

Gly Asp Gly Ser Ser Val Ser Asn Pro Ser Leu Xaa 65 70 75

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<210> 143
<211> 92
<112 - PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (86)
<223> Xaa equals any of the naturally occurring L-amino acids
<400> 143
Met Arg Met Pro Ser His Thr His Ala Arg Phe Val Leu Phe Tyr Leu
                                    10
Ile Leu Arg Asn Arg Ser Gly Gly Val Leu Pro Gly Cys Ser Asp Pro
Glu Gly Ser Gln Glu Ser Pro Gly Leu Gln Lys Ser Pro Pro Thr Gly
Ser Glu Ala Ser Leu Ser Trp Cys Ile Gln Thr Ala His Ser Arg Leu
                          55
 Trp Ala Leu Thr Leu Gln Ile Pro Glu Ser Pro Pro Gly Leu Pro Ala
  65
 Leu Gly Pro Val Pro Xaa Ser Ser Lys Gly Gly Arg
                 85
 <210> 144
 <211> 23
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <223> Xaa equals any of the naturally occurring L-amino acids
 <220>
 <221> SITE
  <222> (23)
  <223> Xaa equals stop translation
  <400> 144
  Met Leu Pro Lys Pro Gln Leu Ser Val Leu Thr Leu Thr Val Ala Leu
```

Ser Xaa Ile Pro Gly Thr Xaa 20

5

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<210> 145
<211> 40
<2112> PRT
<213> Homo sapiens
<2220>
<221> SITE
<222> (40)
<223> Xaa equals stop translation
<40')> 145
Met Glu Met Met Met Val Val Met Gly Cys Val Gln Gly Pro Gly Glu
                       10
 1 5
Gly Cys Scr Gly Lys Met Gly Lys Lys Pro Arg Pro Trp Pro Leu Val
                          25
Ser Tyr Ser Ile Thr His Leu Xaa
        35
 <210> 146
 <211> 35
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (35)
 <223> Xaa equals stop translation
 Met Leu Leu Tyr Gln Ile Asn Ile Pro Phe Ser Phe Ala Leu Ser Val
 1.
 Leu Leu Ser Leu Cys Trp Pro His Gln His Tyr Tyr Pro Cys Tyr Ile
              20
 Ser Phe Xaa
        35
 <210> 147
 <211> 34
  <212> PRT
  <213> Homo sapiens
  <220>
  <231> SITE
  <222> (34)
  <223> Xaa equals stop translation
  Met Cys Val Cys Val Phe Ser Phe Cys Leu Phe Cys Leu Phe Val Phe
                             10
```

```
Gly Met Val Leu Thr Val Leu Cys His Pro Gly Trp Ser Ala Val
                             25
```

Val Xaa

<210> 148

<211> 51

<212> PRT

<?13> Homo sapiens

<220>

<221> SITE

<222> (51)

<223> Xaa equals stop translation

<400> 148

Met Leu Ile Phe Cys Gly Glu Tyr Trp Tyr Phe Cys Phe Asn Leu Leu

Trp Val Val Val Pro Tyr Lys Phe Ser Phe Leu Ser Phe Gly Ser Val 25

Ile Gln Ile Cys Pro Thr Ser Val Pro Pro Ile Gly Gln Ser Gly Ile 40 35

Trp Val Xaa 50

<210> 149

<211> 83

<212> PRT

<213> Homo sapiens

<400> 149

Met Arg Phe Leu Lys Leu Phe Ser His Asn Ile Leu Ile Gln Leu Lys 10

Ile Ile Leu Lys Leu Lys Val Ser Ser Val Leu Pro Ser Val Lys Ser

Leu Lys Asp Glu Arg Ilc Ile Phe Ile Phe Gln Val Ser Leu Asn Lys 35

Val Leu Ser Pro Cys Leu Arg Phe Tyr Pro Gln Arg Thr Ala Thr Phe

Leu Ser Cys Gln Ile Glu Phe Val Gln Gln Leu Arg Asn Thr Gly Lys 75 70

Ile Gln Asn

<222> (73)

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<210> 150
<211> 47
<212> PRT
<213> Homo sapiens
<220>
<0001> SITE
<222> (47)
<223> Xaa equals stop translation
<4.00 > 150
Met Lys Glu Lys Gln Val Tyr His Ile Ser Lys Ile Lys Glu Glu Tyr
                                     10
Ser Ile Leu Ile Cys Leu Leu Ile Val Lys Met Ser Phe Pro Gln Ile
             20
Ala Pro Ile Gln Phe Lys Arg Lys His Ser Thr Lys Ile Gln Xaa
                             40
<210> 151
<211> 49
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (49)
<223> Xaa equals stop translation
<400> 151
Met Trp Asp Gln Arg Pro Thr Lys Gly Thr Gln Asp Phe Gln Leu Leu
                                     10
Leu Leu Pro Gly Ile Cys Ser Ser Phe Ala Leu Leu Leu Asn Ala Leu
             20
Pro Phe Pro Ala Pro Ser Pro Ser Ile Gly Thr Cys Leu Cys Ala Ser
                              40
Xaa
<110> 152
<211> 77
 <212> PRT
<213> Homo sapiens
 <220>
 <221> SITE
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<222> Xaa equals any of the naturally occurring L-amino acids
<2220>
<2221> SITE
<.222→ (77)
<2233> Xaa equals stop translation
<400> 152
Met Gln Trp Val His Ile Ala Glu Thr Gly Asn Glu Lys Phe Ser Phe
Phe Leu Phe Phe Cys Gly Gly Trp Gly Gln Ser Leu Thr Leu Ser
                                 25
             20
Pro Arg Gln Glu Cys Ser Gly Ala Ile Ser Ala His Cys Asn Leu Pro
Pro Pro His Leu Gln Val Gln Ala Ile Leu Val Pro Pro Pro Pro Glu
                        55
Gln Leu Ala Leu Gln Val His Ala Xaa Thr Leu Gly Xaa
                     7.0
 65
<210> 153
<211> 35
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (35)
<223> Xaa equals stop translation
<400> 153
Met Phe Tyr Asp Val Gln Gly Pro Ser His Ser Ser Glu Met Cys Phe
                  5
                                    10
Phe Val Phe Phe Phe Val Cys Leu Phe Leu Phe Leu Met Asn Glu Ser
                                                      30
              20
                                  25
Lys Gly Xaa
<210> 154
 <211> 65
 <211> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (65)
 <223> Xaa equals stop translation
```

<400> 154 Met Val Leu Leu Trp Arg Leu Phe Phe Pro Val Gly Leu Met Arg 10 Ile Ala Gln Pro Leu Gly His Leu Ile Lys His Arg Glu Thr Tyr Ser 25 Leu Arg His Trp Cys Leu His Thr Gln Val Met Leu Gly His Gly Asp 40 Glu Thr Ala Pro Leu Leu Ile Phe Leu Lys Lys Pro Ser Cys His Ile 60 55 Xaa 65 <210> 155 <211> 85 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (85) <223> Xaa equals stop translation <400> 155 Met Ser Ile Gln Val Leu Cys Pro Leu Phe Cys Phe Ala Ser Phe Phe 10 Ile Leu Gly Ser Arg Gly Glu Cys Ala Gly Phe Tyr Thr His Val Leu 20 Gln Asp Pro Arg Ala Trp Ala Ser Asn Asp Pro Ala Thr Gln Val Val Asn Ile Val Pro Asn Arg Glu Phe Ser Thr Leu Ala Leu Leu Pro 55 60 Pro His Phe Trp Asn Pro Trp Cys Pro Leu Phe Pro Cys Cys Ala Met 65 Cys Pro Gln Cys Xaa <210> 156 <211> 3 <212> PRT

<213> Homo sapiens

<220>
<221> SITE
<222> (3)

<400> 159

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<21.3> Xaa equals stop translation
<400> 156
Met Ser Xaa
<210> 157
<211> 42
<212> PRT
<213> Homo sapiens
<400> 157
Met Ala Gly Arg Gly Arg Gly Arg Val Ala Ser Ser Trp Val Gly
Thr Gly Pro Thr Cys Cys Gly Cys Lys Trp Pro Gly Gln Leu Thr Glu
                               25
His Leu Leu Phe Ala Asp Pro Thr Leu Arg
       35
<210> 158
<211> 32
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (32)
<223> Xaa equals stop translation
<400> 158
Met Ser Arg Ala Asn Lys Glu Ile Met Leu Leu Pro Ala Asp Val
                            10
 Pro Leu Val Tyr Ser Val Val Ser Val Gly Arg Val Thr Leu Arg Xaa
                        25
             20
 <210> 159
 <211> 47
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SITE
 <222> (47)
 <223> Xaa equals stop translation
```

Met Trp Asn Phe Ser Cys Ser Thr Ser Ile Cys Glu Tyr Gly Phe Leu 1 5 10 15

Lys Phe Leu Val Leu Tyr Leu Leu Ser Thr Ser Met Ser Ser Pro Leu 20 25 30

Ile Gly Pro Glu Pro His Ser Pro Thr Lys Cys Lys Ile Lys Xaa 35 40 45

<210> 160

<211> 159

<212> PRT

<?13> Homo sapiens

<220>

<0001> SITE

<222> (159)

<2223> Xaa equals stop translation

<400> 160

Met Val Phe Val Val Leu Leu Pro Glu Met Ile Pro Leu Thr Ala Glu
1 5 10 15

Glu Gly Gly Gly Trp Lys Lys Ser Arg Ser Asp Pro Lys Thr Leu Pro

Val Gln Ala Phe Val Phe Lys Cys Gln Ala Trp Gly Pro Arg Arg Arg

Arg Glu Gly Leu Pro Trp Asp Ser Ser Lys Leu Ser Pro Leu Ser Ser 50 55 60

Thr Arg Leu Thr Thr Cys Ser Pro Pro Pro Thr Ser Gly Arg Gly Leu 65 70 75 80

Gln Gly Thr Gln Glu Ala Ala Pro Trp Thr Pro Gly Pro Ser Pro Thr 85 90 95

Lys Pro Ser Val Pro Lys Ala Pro Asp Pro Glu Leu Ala Arg Thr Met 100 105 110

Gln Ala Gly Leu Leu Trp Val Leu Ala Glu Pro Ala Thr Asn Gly Gly 115 120 125

Arg Glu Gly Arg Arg Ser Leu Thr Phe Ser Gln Asn Lys Pro Arg Arg 130 135 140

<210> 161

<211> 90

<212> PRT

```
<213> Homo sapiens
<220>
<211> SITE
<222> (90)
<223> Xaa equals stop translation
<400> 161
Met Val Val Pro Ala Asp Ser Gly Gly Leu Pro Arg Arg Thr Glu Lys
                                     10
Leu Leu Cys Val Met Leu Leu Leu Glu Arg Met Ala Leu Cys Pro
             20
                                 25
Val Leu Asp Val His Thr His Leu Gly Cys Ile Ile Cys Val Ala Cys
Gln Pro Val Arg Thr Val Leu Ser Leu Leu Thr Ala Ser Ile Gln Glu
                        55
Gly Ser Arg Leu Ser Gly His Phe Gln Thr Leu Pro His Gln Thr Asp
65
Thr Thr Phe His Lys Gly Ser Lys Leu Xaa
                 85
<210> 162
<211> 64
<212> PRT
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<210> 162 <211> 64 <212> PRT <213> Homo sapiens <220> <221> SITE

<222> (13)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 162
Met Thr Leu Ile Thr Pro Ala Arg Ile Thr Leu Thr Xaa Gly Asn Lys

1 5 10 15

Ser Trp Ser Ser Thr Ala Val Ala Ala Ala Leu Glu Leu Val Asp Pro

20 25 30

Pro Gly Cys Arg Asn Ser Ala Arg Asp Arg Cys Met His Thr Pro Leu 35 40 45

Cys Val Cys Met Cys Val Cys Val Cys Val Cys Arg Gly Ile Leu Val 50 55 60

```
<211> 146
<212> PRT
<213> Homo sapiens
<320>
<.21> SITE
<.72> (146)
<0.03> Xaa equals stop translation
<400> 163
Met Ser Leu Phe Cys Leu Lys Leu Ser Gly Cys Leu Trp Leu Ser
                                   1.0
Gly Ser Glu Pro His His Gly Leu Gly Phe Leu Leu Trp Pro Leu Ala
            20
                                25
Phe Ala Ser Cys Ser Ile Leu Ile Leu Asn Tyr Ala Lys Pro Phe Leu
                            40
Asn Pro Ala Pro Cys Ser Leu Cys Leu Glu Leu Pro Ser Gln Ala Phe
                        55
Leu Cys Arg Ser Phe Ser Ser His Leu Leu Ser Glu Pro Ser Leu Val
Thr Pro Phe His His Pro Val Cys Phe Leu Pro Ile Ile Trp Phe Pro
Trp Arg Leu Met Ser Val Ser Pro Gln Trp Asn Val Gly Leu Met Ala
          100
                   105
Gln Ala His Arg Gly His Cys Cys Val Gln Gly Ser Val Arg Met Pro
Arg Cys Ala Trp Met Trp Arg Trp Pro Ala Gly Trp Gly Cys His Leu
                       135
                                            140
Ala Xaa
145
<210> 164
<211> 69
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (69)
<2223> Xaa equals stop translation
<400> 164
```

Met Gly Thr Glu Gln Ser Leu Gly Tyr Arg Val Gln Gly Leu Leu

5

Val Leu Ser Leu His Val Ser Gl<br/>n Arg Gly Leu Cys Gly Ser Leu Pro $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Pro Ser Met Ser Ser Glu Glu Arg Lys Gln Arg Pro Trp Ser Ser Gln 35 40 45

Tyr Gly Glu His Cys Val Pro Asp Thr Pro Leu Arg Val Lys Val Arg 50 55 60

Arg His Ile Leu Xaa 65

<210> 165

<211> 89

<212> PRT

<213> Homo sapiens

<400> 165

Met Arg Glu Thr Thr Pro Met Ile Gln Leu Pro Pro Ser Gly Ser Pro
1 5 10 15

Phe Ile Cys Gly Asp Tyr Glu Tyr Tyr His Leu Arg Glu Ile Leu Asn 20 25 30

Gly Ser Thr Asp Pro Asn His Ser Thr Ala Leu Arg Tyr Leu Ile Ile 35 40 45

Lys Leu Pro Lys Val Lys Gly Lys Glu Arg Ile Leu Lys Ile Ala Arg 50 55 60

Glu Lys Lys Gln Ile Thr Cys Asn Gly Ala Pro Ile Cys Leu Ala Ala 65 70 75 80

Asp Val Ser Val Glu Thr Leu Leu Val 85

<210> 166

<211> 88

<212> PRT

<213> Homo sapiens

<400> 166

Met His Phe Trp Thr Gly Pro Arg Phe Gln Leu Gly Leu Ala Gly Val

Pro Ala Ala Gln Phe Glu Thr Ser His Ile Glu Ser Arg Ala Arg Ser 20 25 30

Arg Ala Cys Gly Lys Phe Leu Gly Phe Cys Ser Ser Arg Thr Val Pro 35 40 45

Ser Ala Trp Cys Glu Ala Leu Met Glu Pro Ala Val Ile Gly Tyr Glu 50 55 60

```
Thr Lys Ser Leu Pro Ile His Gly Cys Pro Phe Ile His Trp His Arg
65 70 75 80
```

Thr Pro Gly Thr Asn Glu Gly Asp 85

<210> 167

<211> 37

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (37)

<223> Xaa equals stop translation

<400> 167

Met Leu Asp Pro Ala Ala Ser Gly Thr Phe Arg Ala Leu Leu Leu Leu 1 5 10 15

Ser His Pro Phe Leu Asp Trp Ser Leu Ser Asp Pro His Cys Glu Ser 20 25 30

Leu Asn Gln Lys Xaa 35

<210> 168

<211> 34

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (34)

<223> Xaa equals stop translation

<400> 168

Met Ser His Asn Ile Gln Pro Leu Phe Ser Phe Leu Thr Leu Leu Ser

Tyr Phe Leu Phe His Phe Leu Ser Leu Pro Ser Ser Phe Phe Pro Asn 20 25 30

Tyr Xaa

<210> 169

<211> 36

<212> PRT

<213> Homo sapiens

```
<400> 169
Met Pro Ser Leu Pro Ile Arg Val Thr Lys Phe Ser Glu Ile Gly Asn
```

1 5 10 15

Trp Gln Leu Lys Ala Val Ser Thr Thr Arg Phe Leu Leu Pro Leu Lys 20 25 30

Lys Asn His Phe 35

<210> 170

<211> 57

<212> PRT

<213> Homo sapiens

<400> 170

Met Leu Leu Lys Ser Thr Gly Ser Phe Leu Glu Phe Gly Leu Gln Glu
1 5 10 15

Ser Cys Ala Glu Phe Trp Thr Ser Ala Asp Asp Ser Ser Ala Ser Asp 20 25 30

Glu Ile Arg Leu Glu Leu Cys Phe Leu Ser Pro Ser Thr Ser Tyr Leu 35 40 45

Val Val Ser Phe Leu Met Val Arg Ser 50 55

<210> 171

<211> 45

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (45)

<223> Xaa equals stop translation

<400> 171

Met Tyr Val Lys Ala Ser Ala Val Thr Val Ser Arg Asp Glu Ala Leu 1 5 10 15

Thr Pro Cys Leu Pro Asp Pro His Trp Asn Ala Pro Phe Ala Arg His 20 25 30

Leu Leu Gln Pro Ser Cys Ser Phe Leu Glu Phe Pro Xaa 35 40 45

<210> 172

<211> 96

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (96)

<223> Xaa equals stop translation

<400> 172

Met Leu Ser Glu Thr Pro His Ala Arg Arg Gly Arg Ala Phe Leu Thr
1 5 10 15

Asp Ser Leu Pro Met Val 11e Pro Ser Leu Leu Pro Pro Pro Gly 20 25 30

Arg Ala Ser Leu Ala Glu Pro Thr Leu Arg Ser Val Lys Gly Gln Pro 35 40 45

Leu Thr Leu Ser Gln His Met Glu Asp Leu Ala Val Ser Arg Glu Asn 50 55 60

Cys Ser His Tyr Arg Val Gln Leu Cys Pro Pro Ala Pro Ala Pro Ser 65 70 75 80

Ala Pro Arg Leu Thr Leu Met Ala Leu Ser Cys Ser Ser Leu Pro Xaa 85 90 95

<210> 173

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (49)

<223> Xaa equals stop translation

<400> 173

Met Trp Asp Thr Phe Val Arg Asp Arg Asp Phe Ser Ala Tyr Leu Phe 1 5 10

Leu His Leu Leu Pro Pro Leu Ser Ala Cys Gly Leu Asn Ala Ser Leu 20 25 30

Tyr Thr Ala Thr Pro Ile Val Trp Val Xaa His Thr Ser Pro Gln Asp 35 40 45

Xaa

<210> 174

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<211> 50
<212> PRT
<1.13> Homo sapiens
<120>
<121> SITE
<022> (50)
<223> Xaa equals stop translation
<400> 174
Met Val Arg Ser Ser Ser His Phe Lys Phe Phe Leu Met Leu Phe Thr
                                     10
Ser Thr Leu Gln Asp Val Gly His Thr Ser His Pro Ser Ala Gln Pro
                                25
Ser Ser Arg Leu Ser Asp Ser Pro Leu Ile Cys Leu Ile Asn Arg Gln
                           4.0
Val Xaa
     50
<210> 175
<311> 61
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (61)
<223> Xaa equals stop translation
Met Thr Pro Gly Val Gly Ala Glu Pro Arg Gly Glu Gly Cys Lys Gly
                                      10
Lys Ala Val Arg Gly Leu Gly Gly Glu Arg Val Ser Pro Val Leu Leu
Val Leu His Leu Arg Ser Pro Ser Pro Val Glu Gly Glu Gln Ser Gln
        35
                             40
Arg Gln Trp Gly Val Gln Phe Trp Asn Leu Glu Glu Xaa
                         55
<210> 176
<211> 40
<212> PRT
<213> Homo sapiens
```

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<.1.20>
<22715 SITE
<1.1.2: (15)
<113> Xaa equals any of the naturally occurring L-amino acids
<220>
<121> SITE
<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (40)
<223> Xaa equals stop translation
<400> 176
Ile Leu Gly Phe Ser Phe Ala Val Gly Glu Gly Lys Trp Gly Xaa Phe
                                     10
Cys Leu Leu Val Pro Gly Ile Met Leu His Ile Ile His Leu Leu Ser
                                 25
His Leu Ile Xaa Pro Asn Pro Xaa
         35
<210> 177
<211> 53
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (53)
<223> Xaa equals stop translation
Met Pro Leu Asp Leu Leu Phe Leu Ile Thr Tyr Phe Leu Leu Ser Val
                                      10
Ile Leu Lys Val Leu Tyr Ile Asp Ala Pro Gly His Leu Gly Met Pro
                                  25
Ile Ser Leu Cys Ser Ser Ala Val Val Trp Val Lys Val Asp Leu Val
                             40
        35
Ser Glu Lys Gly Xaa
     50
<210> 178
<211> 41
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SITE
<1.22> (41)
<223> Xaa equals stop translation
<400> 178
Met Ser Val Leu Ser Gly Phe Leu Phe Ile Val Val Cys Cys Tyr
                5
                                    1.0
Cys Cys Phe Val Ala Arg Leu Gln Leu Thr Lys Tyr Glu Phe Lys Asn
                                 25
Cys Val Val Ile Phe Arg Asp Leu Xaa
<210> 179
<211> 105
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (105)
<223> Xaa equals stop translation
<400> 179
Met Glu Arg Asp Thr Arg Glu Lys Cys Leu Trp Ser Leu Pro Tyr Pro
                                    10
Lys Leu Cys Asn Leu Leu Ala Ser His Phe Leu Ser Ile Leu Ser
             20
Phe Phe Ile Tyr Ser Ile Gly Phe Leu Asp Leu Val Val Ser Asn Thr
Leu Pro Val Phe Gln Phe Asp Val Thr Phe Tyr Pro Val Thr Lys Phe
                         55
Ile Phe Gln Lys His Ser Met Leu Cys His Thr Ala Asn Leu Val Asn
                    70
 65
Val Pro Asp Met Val Trp Leu Cys Pro His Pro Asn Leu Ile Leu Asn
                 85
                                     90
Cys Ser Ser His Asn Pro His Met Xaa
            100
                                105
```

<210> 180 <211> 40

<212> PRT

<213> Homo sapiens

```
<220>
<221> SITE
<222> (40)
<223> Xaa equals stop translation
<400> 180
Met Asp Tyr Glu Val Ile Ser Gln Asn Val Arg Lys Arg Tyr Arg Ala
                      10
Leu Glu Leu Leu Tyr Leu Leu Leu Asn Leu Asn Ile Thr Ala Thr Asn
                    25
            20
Lys Gly Tyr Gln Asp Lys Val Xaa
       35
<210> 181
<211> 25
<212> PET
<213> Homo sapiens
<220>
<221> SITE
<222> (25)
<223> Xaa equals stop translation
<400> 181
Met Ile Tyr Phe Leu Leu Leu Pro Glu Ala Gln Gly Glu Phe Ser
               5
                            10
Ser Ile Phe Thr Val Arg Thr Trp Xaa
            20
<210> 182
<211> 54
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids
<200>
<121> SITE
<2000> (54)
<223> Xaa equals stop translation
<400> 182
Met Cys Pro Pro Ser Gln Arg Ala Pro Thr His Leu Xaa Cys Pro Trp
                         10
 Val Asp Pro Gly Pro Val Val Leu Gly Leu Ser Leu Trp Val Leu Ala
            20 25 30
```

```
Gly Gly Met Gly Glu Gly Glu Gln Leu Pro Ala Pro Leu Leu Cys
                            40
Gly Ser Ser Phe Phe Xaa
   50
<210> 183
<211> 66
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (50)
<2003> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (66)
<223> Xaa equals stop translation
<400> 183
Met Leu Leu Asn Thr Ser Phe Thr Arg Glu Ile Ile Ser Gln Arg
                                                        15
                5
                                    10
Glu Ser Asn Trp Leu Val Leu Leu Leu Leu Phe Phe Pro Val Ile
                                25
Cys Phe Ile Glu Arg Ser Leu Cys Gly Gly Thr Asp Phe Leu Asn Thr
                            40
Leu Xaa His Thr His Thr Tyr Thr Pro Ser Ile Tyr Gly Ala Met His
     50
                        55
Arg Xaa
 65
<210> 184
<211> 27
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<222> (27)
<223> Xaa equals stop translation
<400> 184
Met Ile His Leu Ser Arg Phe Tyr Leu Leu Leu Ile Met Leu Pro His
                                    10
Val Leu Phe Phe Thr Gly Asp Leu His Ser Xaa
```

20 25 <210> 185 <211> 24 <1.12> PRT <1113> Homo sapiens <220> <221> SITE <222> (24) <223> Xaa equals stop translation <400> 185 Met Phe Pro Phe Pro Phe His Leu Val Ile Leu Gly Phe Leu Leu 10 1 Leu His Ser Phe Leu Pro Pro Xaa 20 <210> 186 <211> 42 <212> PRT <113> Homo sapiens <220> <221> SITE <222> (42) <223> Xaa equals stop translation <400> 186 Met Ser Gln Thr Leu Val Ala Leu Pro Glu Arg Asn Glu Asn Ala Gln Pro His Pro Cys Thr Leu Cys Ser Phe Leu Phe Asn Thr Glu Glu Pro 20 25 Glu Trp Arg Gly Pro Ala Gly Leu Gln Xaa <210> 187 <211> 223 <312> PRT <213> Homo sapiens <220>

<220>
<221> SITE
<222> (75)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (146)

<323> Xaa equals any of the naturally occurring L amino acids

<2230>

<221> SITE

<222> (159)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 187

Met Val Pro Arg Thr Ser His Thr Ala Ala Phe Leu Ser Asp Thr Lys

1 5 10 15

Asp Arg Gly Pro Pro Val Gln Ser Gln Ile Trp Arg Ser Gly Glu Lys
20 25 30

Val Pro Phe Val Gln Thr Tyr Ser Leu Arg Ala Phe Glu Lys Pro Pro 35 40 45

Gln Val Gln Thr Gln Ala Leu Arg Asp Phe Glu Lys His Leu Asn Asp 50 55 60

Leu Lys Lys Glu Asn Phe Ser Leu Lys Leu Xaa Ile Tyr Phe Leu Glu 65 70 75 80

Glu Arg Met Gln Gln Lys Tyr Glu Ala Ser Arg Glu Asp Ile Tyr Lys 85 90 95

Arg Asn Thr Glu Leu Lys Val Glu Val Glu Ser Leu Lys Arg Glu Leu 100 105 110

Gln Asp Lys Lys Gln His Leu Asp Lys Thr Trp Ala Asp Val Glu Asn 115 120 125

Leu Asn Ser Gln Asn Glu Ala Glu Leu Arg Arg Gln Phe Glu Glu Arg 130 135 140

Leu Leu Gln Glu Glu Ser Arg Leu Ala Lys Asn Glu Ala Ala Arg Met 165 170 175

Ala Ala Leu Val Glu Ala Glu Lys Glu Cys Asn Leu Glu Leu Ser Glu
180 185 190

Lys Leu Lys Gly Val Thr Lys Asn Trp Glu Asp Val Pro Gly Asp Gln
195 200 205

Val Lys Pro Asp Gln Tyr Thr Glu Ala Leu Ala Gln Arg Asp Lys 210 215 220

<210> 188

<211> 239

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (91)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<331> SITE

<332> (162)

<2003> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (175)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 188

Met Glu Gln Thr Trp Thr Arg Asp Tyr Phe Ala Glu Asp Asp Gly Glu 1.0

Met Val Pro Arg Thr Ser His Thr Ala Ala Phe Leu Ser Asp Thr Lys

Asp Arg Gly Pro Pro Val Gln Ser Gln Ile Trp Arg Ser Gly Glu Lys 40

Val Pro Phe Val Gln Thr Tyr Ser Leu Arg Ala Phe Glu Lys Pro Pro 60 55

Gln Val Gln Thr Gln Ala Leu Arg Asp Phe Glu Lys His Leu Asn Asp 65

Leu Lys Lys Glu Asn Phe Ser Leu Lys Leu Xaa Ile Tyr Phe Leu Glu 90

Glu Arg Met Gln Gln Lys Tyr Glu Ala Ser Arg Glu Asp Ile Tyr Lys 100

Arg Asn Thr Glu Leu Lys Val Glu Val Glu Ser Leu Lys Arg Glu Leu 120

Gln Asp Lys Lys Gln His Leu Asp Lys Thr Trp Ala Asp Val Glu Asn 135

Leu Asn Ser Gln Asn Glu Ala Glu Leu Arg Arg Gln Phe Glu Glu Arg 150 145

His Xaa Glu Thr Glu His Val Tyr Glu Leu Leu Glu Asn Lys Xaa Gln 170 165

Leu Leu Gln Glu Glu Ser Arg Leu Ala Lys Asn Glu Ala Ala Arg Met 180 185

Ala Ala Leu Val Glu Ala Glu Lys Glu Cys Asn Leu Glu Leu Ser Glu 205 200 195

Lys Leu Lys Gly Val Thr Lys Asn Trp Glu Asp Val Pro Gly Asp Gln 210 215 220

Val Lys Pro Asp Gln Tyr Thr Glu Ala Leu Ala Gln Arg Asp Lys 225 230 235

<210> 189

<211> 228

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (66)

<2223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (127)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (131)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (141)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 189

Ile Arg His Glu Leu Leu Pro Ala Leu His Leu Gln Ala His Asp Ala

1 5 10 15

Ala Tyr Asn Leu Leu Phe Phe Ala Ser Gly Gly Gly Lys Phe Asn Tyr 20 25 30

Gln Gly Thr Lys Arg Trp Leu Glu Asp Asn Leu Asp His Thr Gly Glu 35 40 45

Arg Pro Arg Val Gly Val Gly Val Pro Arg Trp Trp Cys Arg Gly Glu
50 55 60

Ala Xaa Arg Pro Arg Gly Cys His Gly Gly Ser Gln Glu Ala Gln Arg 65 70 75 80

Glu Gly Arg Gly Pro Leu Pro Gly Pro His Pro Pro Arg Gln Leu Ser 85 90 95

Val Ser Cys Arg Leu Gln Pro Ala Ser Gly Gln Cys Gly Leu Arg Ala 100 105 110 Val Pro Gly His Arg Gly Pro Gly Gln Gln Pro Ala Pro Ala Xaa Val 115 120 125

Arg Pro Xaa Arg Glu Gly Thr Leu Gln His Ala Phe Xaa Arg Glu Leu 130 135 140

His Lys Arg Ile Asn Leu Ala Glu Asp Val Leu Ala Trp Glu His Glu 165 170 175

Arg Phe Ala Ile Arg Arg Leu Pro Ala Phe Thr Leu Ser His Leu Glu 180 185 190

Ser His Arg Asp Gly Gln Arg Ser Ser Ile Met Asp Val Arg Ser Arg 195 200 205

Val Asp Ser Lys Thr Leu Ile Arg Leu Pro Gln Pro Pro Lys Val Leu 210 215 220

Gly Leu Arg Val 225

<210> 190

<111> 40

<212> PRT

<213> Homo sapiens

<400> 190

Ile Tyr Leu Asn Ile Gln Val Val Arg Gly Gln Arg Lys Val Ile Cys
1 5 10 15

Leu Leu Lys Glu Gln Ile Ser Asn Glu Gly Glu Asp Lys Ile Phe Leu 20 25 30

Ile Asn Lys Leu His Ser Ile Tyr
35 40

<210> 191

<211> 27

<212> PRT

<213> Homo sapiens

<400> 191

Glu Arg Lys Glu Arg Glu Glu Arg Ser Arg Val Gly Thr Thr Glu Glu
1 5 10 15

Ala Ala Ala Pro Pro Ala Leu Leu Thr Asp Glu 20 25

```
<211> 7
<212> PRT
<113> Homo sapiens
<400> 192
Arg His Glu Met Glu Asn Thr
5
<210> 193
<211> 53
<212> PRT
<213> Homo sapiens
<400> 193
Arg Lys Leu Ser Thr Gly Pro Phe Ser Ala Cys Lys Pro Arg Ala Thr
1 5 10 15
Cys Cys Phe Thr Ser Cys Tyr Leu Gln Gln Leu Leu Asp Ala Thr Glu
                            25
Asp Gly His Pro Pro Lys Gly Lys Ala Ser Ser Leu Ile Pro Thr Cys
                         40
Leu Lys Ile Leu Gln
  50
<210> 194
<211> 29
<212> PRT
<213> Homo sapiens
<400> 194
Thr Ser Cys Tyr Leu Gln Gln Leu Leu Asp Ala Thr Glu Asp Gly His
 Pro Pro Lys Gly Lys Ala Ser Ser Leu Ile Pro Thr Cys
           20 25
 <210> 195
 <211> 25
 <212> PRT
 <213> Homo sapiens
 <400> 195
 Cys Cys Gly Ala Lys Arg Ile Met Lys Glu Ala Leu His Trp Ala Leu
 Phe Ser Met Gln Ala Thr Gly His Val
           20
```

<211> 196 <212> PRT <213> Homo sapiens <2220> <2:21> SITE <222> (13) <:23> Xaa equals any of the naturally occurring L-amino acids <220> <001> SITE <222> (15) <223> Xaa equals any of the naturally occurring L-amino acids <220> <221> SITE <222> (91) <223> Xaa equals any of the naturally occurring L-amino acids <220> <221> SITE <222> (126) <223> Xaa equals any of the naturally occurring L-amino acids <400> 196 Pro Pro Ala Gly Ala Thr Ser Pro Gly Arg Ile Ile Xaa Pro Xaa Ser Ala Val Leu Ile Pro Ser Pro Val Lys Ser Tyr Arg Gly Trp Leu Val 20 25 Met Gly Glu Pro Ser Arg Glu Glu Tyr Lys Ile Gln Ser Phe Asp Ala Glu Thr Gln Gln Leu Leu Lys Thr Ala Leu Lys Asp Pro Gly Ala Val 55 Asp Leu Glu Lys Val Ala Asn Val Ile Val Asp His Ser Leu Gln Asp 65 Cys Val Phe Ser Lys Glu Ala Gly Arg Met Xaa Tyr Ala Ile Ile Gln 90 Ala Glu Ser Lys Gln Ala Gly Gln Ser Val Phe Arg Arg Gly Leu Leu 105 100 Asn Arg Leu Gln Gln Glu Tyr Gln Ala Arg Glu Gln Leu Xaa Ala Arg 120 115 Ser Leu Gln Gly Trp Val Cys Tyr Val Thr Pne Ile Cys Asn Ile Phe 140 135 Asp Tyr Leu Arg Val Asn Asn Met Pro Met Met Ala Leu Val Asn Pro

150 155

145

160

```
Val Tyr Asp Cys Leu Phe Arg Leu Ala Gln Pro Asp Ser Leu Ser Lys
                                                   175
                      170
              165
Glu Glu Glu Val Asp Cys Leu Val Leu Gln Leu His Arg Vai Gly Glu
                              185
           180
Gln Leu Glu Lys
      195
<210> 197
<211> 24
<212> PRT
<213> Homo sapiens
<220>
<221> SITE
<322> (6)
<223> Xaa equals any of the naturally occurring L-amino acids
<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids
<400> 197
Pro Gly Arg Ile Ile Xaa Pro Xaa Ser Ala Val Leu Ile Pro Ser Pro
Val Lys Ser Tyr Arg Gly Trp Leu
             20
 <210> 198
 <211> 25
 <212> PRT
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 Gln Gln Glu Tyr Gln Ala Arg Glu Gln
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Ala Gly Xaa Ser Gln Gln Pro Leu Ser Leu Asp Ser Glu Ala Pro Arg 20 25 30

Gly Gly Val Ala Pro Pro Arg Leu Gln Gly Pro Pro Pro His Gln Arg
35 40 45

Val His Leu Thr Leu Glu Cys Thr Thr His Pro Thr Val Gly Lys Ala 50 55 60

Ser Val Leu Gly Pro Cys Leu Leu Leu Leu Ser Cys Pro Arg Ala Pro 65 70 75 80

Ala Gly Pro Pro Pro Pro Pro His Ser Arg Val Arg Ala Gly Gly Cys
85 90 95

Arg Pro Trp Ala Arg Arg Glu Gly His Cys Arg Pro Leu Gly Ala Asp 100 105 110

Thr Asp Thr Ser Arg Ile Cys His Gly Arg Arg Pro Phe Ser Leu 115 120 125

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Met Ser Leu Pro Ala Ala Pro Ala Gly Arg Leu Ser Pro Leu Tyr Trp 1 5 10 15

Arg Ser Ser Asn Thr Arg Ser Gln Leu Ser Leu Leu Trp Glu Leu Gly
20 25 30

His Phe Phe Thr Arg Cys Cys Arg Arg Pro His Pro Asn Pro His Leu 35 40 45

Pro Ala Leu Ser Val Cys Arg Cys His Ile Leu His Lys Ile Met Leu  $50 \,$   $\,$   $55 \,$   $\,$   $60 \,$ 

Trp Glu Pro Ser Ser Pro Leu Leu Pro Ala Leu Pro
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1 5 10 15

Ser His Asn Met Ile Leu Cys Lys Ile Trp Gln Arg His Thr Leu Arg

Ala Gly Arg Trp Gly Leu Gly Trp Gly Arg Arg Gln His Arg Val Lys
35 40 45

Lys Cys Pro Ser Ser His Ser Lys Glu Ser Cys Asp Arg Val Phe Glu 50 55 60

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Leu

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<213> Homo sapiens
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Gln Gly Asn Gly Val Leu Asn Ser Arg Asp Ala Ala Arg His Thr Ala 20 25 30

Gly Ala Lys Arg Tyr Lys Tyr Leu Arg Arg Leu Phe Arg Phe Arg Gln

Met Asp Phe Glu Phe Ala Ala Trp Gln Met Leu Tyr Leu Phe Thr Ser 50 60

Pro Gln Arg Val Tyr Arg Asn Phe His Tyr Arg Lys Gln Thr Lys Asp 65 70 75 80

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<211> 117

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<.213> Homo sapiens

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Gln Leu Phe Phe Ile Asn His Val Ile Leu Thr Asp Thr Phe Ile Gly 35 40 45

Tyr Leu Val Gly Asn Thr Leu Trp Leu Val Ala Val Gly Tyr Tyr Ile
50 55 60

Tyr Val Thr Phe Leu Gly Tyr Ser Ala Leu Pro Phe Leu Lys Asn Thr 65 70 75 80

Val Ile Leu Leu Tyr Pro Phe Ala Pro Leu Ile Leu Leu Tyr Gly Leu 85 90 95

Ser Leu Ala Leu Gly Trp Asn Phe Thr His Thr Leu Cys Ser Phe Tyr 100 105 110

Lys Tyr Arg Val Lys 115

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<213> Homo sapiens

<400> 209

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Leu Phe Arg Phe Arg Gln Met Asp Phe Glu Phe Ala Ala 35 40 45

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Asp Met Met Pro
   20
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<210> 216

<311> 153

<212> PRT

<213> Homo sapiens

<400> 216

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1 5 10 15

Val Pro Glu Thr Pro Asp Asn Glu Arg Lys Ala Ser Ile Ser Tyr Phe
20 25 30

Lys Asn Gln Arg Gly Ile Gln Tyr Ile Asp Leu Ser Ser Asp Ser Glu 35 40 45

Asp Val Val Ser Pro Asn Cys Ser Asn Thr Val Gln Glu Lys Thr Phe 50 55 60

Asn Lys Asp Thr Val Ile Ile Val Ser Glu Pro Ser Glu Asp Glu Glu 65 70 75 80

Ser Gln Gly Leu Pro Thr Met Ala Arg Arg Asn Asp Asp Ile Ser Glu 85 90 95

Leu Glu Asp Leu Ser Glu Leu Glu Asp Leu Lys Asp Ala Lys Leu Gln 100 105 110

Thr Leu Lys Glu Leu Phe Pro Gln Arg Ser Asp Asn Asp Leu Leu Lys
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<211> 16
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Glu Asp Ser Ser Val Pro Glu Thr Pro Asp Asn Glu Arg Lys Ala Ser 10

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## **CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

## **NORWAY**

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

### **AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

#### **FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

## UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

## Page 2

#### DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later that at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

#### **SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

## **NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

# INTERNATIONAL SEARCH REPORT

International application No. PCT/US98/15949

| IPC(6) :C                      | SIFICATION OF SUBJECT MATTER<br>07H 19/00; C12P 19/34; C12Q 1/68<br>536/22.1; 435/91.41; 435/6<br>International Patent Classification (IPC) or to both nati   | onal classification and IPC   |
|--------------------------------|---|---|
|                                |   |   |
| FIELD                          | S SEARCHED cumentation searched (classification system followed by  | classification symbols)   |
|                                |   |   |
|                                | 536/22.1; 435/91.41; 435/6  | 1 1 1 at a Colde coambed  |
| Documentation                  | on searched other than minimum documentation to the ex  | tent that such documents are included in the fields searched  |
|                                | ata base consulted during the international search (name  | e of data base and, where practicable, search terms used)   |
| C. DOC                         | UMENTS CONSIDERED TO BE RELEVANT  |   |
| Category*                      | Citation of document, with indication, where appre  | opriate, of the relevant passages Relevant to claim No.   |
| Y                              | STEWART et al. Growth, Differentiati  | on, and survival: Multiple 1-23   |
| Y                              | JOHNSTONE et al. Immunochemis<br>Blackwell Scientific Publications. secon   | try in Practice. London: 1-23 and edition, 1987, page 30.   |
| · s                            | ther documents are listed in the continuation of Box C.  Special categories of cited documents:  Social categories of cited documents:  Social categories of cited documents and considered on the special categories are considered on the special categories. | err later document published after the international filing date on process date and not in conflict with the application but cited to understand the principle or theory underlying the invention        |
| •E• •                          | arlier document published on or after the international filing date   | when the document is taken alone  |
| c                              | locument which may undow doubt of another citation or other itself to establish the publication date of another citation or other pecial reason (as specified)  locument referring to an oral disclosure, use, exhibition or other                              | "Y" document of particular relevance; the claimed invention cannot be<br>considered to involve an inventive step when the document is<br>combined with one or more other such documents, such combination |
| 1 2                            | neans   | being obvious to a person skilled in the art  document member of the same patent family   |
| l t                            | ocument published prior to the international filing date but later than the priority date claimed   | Date of mailing of the international search report  |
| 1                              | e actual completion of the international search OBER 1998   | 16 DEC 1998   |
| Name and<br>Commiss<br>Box PCT | I mailing address of the ISA/US<br>tioner of Patents and Trademarks   | Authorized officery EGGERTON CAMPBELL (703) 208 0196  |
|                                | No. (703) 305-3230  | Telephone No. (703) 308-0196  |

## INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/15949

|           | tion). DOCUMENTS CONSIDERED TO BE RELEVANT   | Relevant to claim No. |
|-----------|--|-----------------------|
| Category* | Citation of document, with indication, where appropriate, of the relevant passages   |                       |
| Y         | SKONIER et al. Big-h3: A Transforming Growth Factor-B-Responsive Gene Encoding a Secreted Protein That Inhibits Cell Attachment In Vitro and Suppresses the Growth of CHO Cells in Nude Mice. DNA and Cell Biology. 1994, Vol. 13, No. 6, pages 571-584, see entire article. | 1-23                  |
| Y         | XUAN et al. Recombinant PSP94 Demonstrates Similar Linear<br>Epitote Structure as Natural PSP94 Protein. J. Cellular<br>Biochemistry. 1996, Vol. 63, pages 61-73, see entire article.  | 1-23                  |
| Y         | EP 0 559 428 A2 (ONO PHARMACEUTICAL CO, LTD.1) 08<br>September 1993, see entire document.  | 1-23                  |
| Y         | LEWIS et al Rescue, Expression, and Analysis of a Neutralizing Human Anti-Hepatitis A Virus Monoclonal Antibody. J. Immunology. 01 September 1993, Vol. 151, No. 5, pages 2829-2838, see entire article.   | 1-23                  |
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|           |  |                       |